86136

Access DB# _____ LB

SEARCH REQUEST FORM

CRFE

Scientific and Technical Information Center

Requester's Full Name: Lisa V. Cook Examiner #: 77134 Date: 2/5/03
Art Unit: 1641 Phone Number 305-0808 Serial Number: 09/845,729
Mail Box and Bldg/Room Location: CM1-7E12 Results Format Preferred (circle): PAPER DISK E-MAIL
Office CM1 7B-17

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Biopolymer marker indicative of disease state having a molecular weight of 1350 daltons.
Inventors (please provide full names): George Jackowski, Brad Thatcher, John Marshall, Tammy Vrees
Earliest Priority Filing Date: 4/30/01

For Sequence Searches Only *Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Sequence Search for: SESIDF LAE GGGVR
Seq. Id. No. 1

Sequence utility in detecting myocardial infarction or renal failure. Biopolymer marker/antibodies/ assay

also see attached claims + bib sheet

Thanks, :)
L Cook

RECEIVED FEB-6 2003 TECH CENTER 1600/2900

alg 1 AA @ 13

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

****

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: Beverly c4994	NA Sequence (#):	STN ✓
Searcher Phone #:	AA Sequence (#)	Dialog
Searcher Location:	Structure (#)	Questel/Orbit
Date Searcher Picked Up:	Bibliographic	Dr.Link
Date Completed: 02-11-03	Litigation	Lexis/Nexis
Searcher Prep & Review Time: 3	Fulltext	Sequence Systems
Clerical Prep Time:	Patent Family	WWW/Internet
Online Time: 21	Other	Other (specify) CGN

PTO-1590 (8-01)

Cook, L.
09/845729

FILE 'REGISTRY' ENTERED AT 09:18:47 ON 11 FEB 2003
L1 2 S SESDFLAEGGGVR/SQSP

L1 ANSWER 1 OF 2 REGISTRY COPYRIGHT 2003 ACS
RN 474451-10-0 REGISTRY
CN Glycine, L-.alpha.-aspartyl-L-seryl-L-.alpha.-glutamyl-L-seryl-L-.alpha.-aspartyl-L-phenylalanyl-L-leucyl-L-alanyl-L-.alpha.-glutamylglycylglycylglycyl-L-valyl-L-arginyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 7: PN: US20020160420 PAGE: 12 unclaimed sequence
SQL 15

SEQ 1 DSESDFLAEG GGVRG
========== ====
HITS AT: 2-14

REFERENCE 1: 137:348834

L1 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2003 ACS
RN 473552-35-1 REGISTRY
CN L-Arginine, L-seryl-L-.alpha.-glutamyl-L-seryl-L-.alpha.-aspartyl-L-phenylalanyl-L-leucyl-L-alanyl-L-.alpha.-glutamylglycylglycylglycyl-L-valyl- (9CI) (CA INDEX NAME)
SQL 13

SEQ 1 SESDFLAEGG GVR
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HITS AT: 1-13

REFERENCE 1: 137:334901

FILE 'HCAPLUS' ENTERED AT 09:19:16 ON 11 FEB 2003
L2 2 S L1

L2 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:833425 HCAPLUS
DOCUMENT NUMBER: 137:334901
TITLE: Alpha fibrinogen biopolymer marker indicative of myocardial infarction or renal failure having a molecular weight of 1350 daltons
INVENTOR(S): Jackowski, George; Thatcher, Brad; Marshall, John; Yantha, Jason; Vrees, Tammy
PATENT ASSIGNEE(S): Can.
SOURCE: U.S. Pat. Appl. Publ., 10 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002160528	A1	20021031	US 2001-845729	20010430
WO 2002088722	A2	20021107	WO 2002-CA610	20020426
WO 2002088722	A3	20021227		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,

LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2001-845729 A 20010430

AB The instant invention involves the use of a combination of preparatory steps in conjunction with mass spectroscopy and time-of-flight detection procedures to maximize the diversity of biopolymers which are verifiable within a particular sample. The cohort of biopolymers verified within such a sample is then viewed with ref. to their ability to evidence at least one particular disease state; thereby enabling a diagnostician to gain the ability to characterize either the presence or absence of said at least one disease state relative to recognition of the presence and/or the absence of said biopolymer. Serum samples were analyzed by SELDI-TOF using the Ciphergen PROTEINCHIP system and the disease specific marker identified by the sequence SESDFLAEGGGVR and characterized as a .alpha. fibrinogen having a mol. wt. of 1350 daltons was found. This marker is indicative of myocardial infarction or renal failure.

IT **473552-35-1**
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(alpha fibrinogen biopolymer marker of 1350 daltons indicative of myocardial infarction or renal failure)

L2 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:833395 HCAPLUS
DOCUMENT NUMBER: 137:348834
TITLE: Process for diagnosis of physiological conditions by characterization of proteomic materials
INVENTOR(S): Jackowski, George; Thatcher, Brad; Marshall, John; Yantha, Jason; Vrees, Tammy
PATENT ASSIGNEE(S): Can.
SOURCE: U.S. Pat. Appl. Publ., 25 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002160420	A1	20021031	US 2001-846330	20010430
WO 2002088744	A2	20021107	WO 2002-CA623	20020429

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2001-846330 A 20010430

AB The present invention discloses the use of proteomic investigation as a diagnostic tool; and particularly teaches the use of proteomic investigative techniques and methodol. to det. a proteomic basis for the development and progression of abnormal physiol. conditions and the development and characterization of risk assessment, diagnostic and therapeutic means and methodologies. Serum samples from patients suffering from a variety of diseases in Syndrome X were analyzed by SELDI mass spectrometry using the Ciphergen PROTEINCHIP system to discern disease markers.

IT **474451-10-0**
RL: PRP (Properties)
(unclaimed sequence; process for diagnosis of physiol. conditions by characterization of proteomic materials)

FILE 'HOME' ENTERED AT 09:19:25 ON 11 FEB 2003

Cook, L.
09/845729
Seq. ID 1 w/
Interf

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 16:00:57 ; Search time 354 Seconds
(without alignments)
23.677 Million cell updates/sec

Title: US-09-845-729-1
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
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26: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	87.7	12	22	US-09-845-725-1	Sequence 1, Appli
2	57	87.7	15	22	US-09-845-719A-1	Sequence 1, Appli
3	57	87.7	16	1	PCT-US99-03350A-25	Sequence 25, Appl
4	57	87.7	16	8	US-08-469-141-56	Sequence 56, Appl
5	57	87.7	16	12	US-08-844-462-14	Sequence 14, Appl
6	57	87.7	16	14	US-09-025-319A-25	Sequence 25, Appl
7	57	87.7	16	19	US-09-525-269-25	Sequence 25, Appl
8	57	87.7	16	20	US-09-622-561-25	Sequence 25, Appl
9	57	87.7	16	20	US-09-648-816-25	Sequence 25, Appl
10	57	87.7	16	20	US-09-648-816A-25	Sequence 25, Appl
11	57	87.7	16	20	US-09-648-816A-109	Sequence 109, App
12	57	87.7	16	20	US-09-648-816B-25	Sequence 25, Appl
13	57	87.7	16	20	US-09-657-276-1135	Sequence 1135, Ap
14	57	87.7	16	22	US-09-826-290-352	Sequence 352, App
15	57	87.7	16	22	US-09-845-765-1	Sequence 1, Appli
16	57	87.7	16	22	US-09-846-780-1	Sequence 1, Appli
17	57	87.7	17	1	PCT-US02-14741-10	Sequence 10, Appl
18	57	87.7	17	1	PCT-US02-22821-53	Sequence 53, Appl
19	57	87.7	17	8	US-08-469-141-46	Sequence 46, Appl
20	57	87.7	17	20	US-09-657-276-1136	Sequence 1136, Ap
21	57	87.7	17	25	US-10-142-935-10	Sequence 10, Appl
22	57	87.7	17	25	US-10-197-954-53	Sequence 53, Appl
23	57	87.7	18	8	US-08-469-141-55	Sequence 55, Appl
24	57	87.7	19	8	US-08-469-141-54	Sequence 54, Appl
25	57	87.7	20	1	PCT-US99-03350A-26	Sequence 26, Appl
26	57	87.7	20	8	US-08-469-141-53	Sequence 53, Appl
27	57	87.7	20	8	US-08-478-260-1	Sequence 1, Appli
28	57	87.7	20	8	US-08-480-126-1	Sequence 1, Appli
29	57	87.7	20	8	US-08-483-990-1	Sequence 1, Appli
30	57	87.7	20	14	US-09-025-319A-26	Sequence 26, Appl
31	57	87.7	20	19	US-09-525-269-26	Sequence 26, Appl
32	57	87.7	20	20	US-09-622-561-26	Sequence 26, Appl
33	57	87.7	20	20	US-09-648-816-26	Sequence 26, Appl
34	57	87.7	20	20	US-09-648-816A-26	Sequence 26, Appl
35	57	87.7	20	20	US-09-648-816A-110	Sequence 110, App
36	57	87.7	20	20	US-09-648-816B-26	Sequence 26, Appl
37	57	87.7	21	8	US-08-469-141-45	Sequence 45, Appl
38	57	87.7	22	8	US-08-469-141-44	Sequence 44, Appl
39	57	87.7	22	8	US-08-469-141-52	Sequence 52, Appl
40	57	87.7	25	21	US-09-757-774-16	Sequence 16, Appl
41	57	87.7	30	3	US-07-963-538-9	Sequence 9, Appli
42	57	87.7	30	14	US-09-086-664-9	Sequence 9, Appli
43	57	87.7	30	14	US-09-087-371-9	Sequence 9, Appli
44	57	87.7	44	27	US-60-160-203-3985	Sequence 3985, Ap
45	57	87.7	360	1	PCT-US00-05989-587	Sequence 587, App

ALIGNMENTS

RESULT 1
US-09-845-725-1
; Sequence 1, Application US/09845725
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 1206 DALTONS
; FILE REFERENCE: 2132.028
; CURRENT APPLICATION NUMBER: US/09/845,725
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-725-1

Query Match 87.7%; Score 57; DB 22; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 ESDFLAEGGGVR 13
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Db       1 EGDFLAEGGGVR 12
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RESULT 2
US-09-845-719A-1

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; Sequence 1, Application US/09845719A
; GENERAL INFORMATION:
;  APPLICANT: Jackowski, George
;  TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
;  TITLE OF INVENTION:  OF 1465 DALTONS
;  FILE REFERENCE: 2132.035
;  CURRENT APPLICATION NUMBER: US/09/845,719A
;  CURRENT FILING DATE:  2001-04-30
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-845-719A-1

  Query Match             87.7%;  Score 57;  DB 22;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 0.012;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
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Db      4 EGDFLAEGGGVR 15


RESULT 3
PCT-US99-03350A-25
; Sequence 25, Application PC/TUS9903350A
;  GENERAL INFORMATION:
;    APPLICANT:  Yeaman, Michael R.
;    APPLICANT:  Shen, Alexander J.
;    TITLE OF INVENTION:  Antimicrobial Peptides And Derived Metapeptides
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FULWIDER PATTON LEE & UTECHT, LLP
;      STREET:  10877 Wilshire Blvd., Tenth Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90024
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  Hewlett Packard
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US99/03350A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/025,319
;      FILING DATE:  February_18, 1998.
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Drucker, I. Morley
;      NAME:  Parkhurst, David G.
;      REGISTRATION NUMBER:  19,751
;      REGISTRATION NUMBER:  29,422
;      REFERENCE/DOCKET NUMBER:  REI 50480
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (310) 824-5555
;      TELEFAX:  (310) 824-9696
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    FRAGMENT TYPE:  internal fragment
;    FEATURE:
;      NAME/KEY:  CS-FBP"
;      IDENTIFICATION METHOD:  By experiment
;      OTHER INFORMATION:  microbicidal activities,
;      OTHER INFORMATION:  PMIC = -78.53; MW = 1806.90; number of charged amino acids:
PCT-US99-03350A-25

  Query Match             87.7%;  Score 57;  DB 1;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 4
US-08-469-141-56
; Sequence 56, Application US/08469141
;  GENERAL INFORMATION:
;    APPLICANT:  MUMFORD, RICHARD A.
;    APPLICANT:  DAVIES, D.T. PHILIP
;    APPLICANT:  DAHLGREN, MARY E.
;    APPLICANT:  BOGER, JOSHUA S.
;    APPLICANT:  HUMES, JOHN L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DR. CHRISTINE E. CARTY
;      STREET:  126 E. LINCOLN AVENUE., P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,141
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARTY, CHRISTINE E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)-594-6734
;      TELEFAX:  (908)-594-4720
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-469-141-56

  Query Match             87.7%;  Score 57;  DB 8;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 5
US-08-844-462-14
; Sequence 14, Application US/08844462
;  GENERAL INFORMATION:
;    APPLICANT:  PATTERSON, DALE H.
```

```
;    APPLICANT:  TARR, GEORGE E.
;    TITLE OF INVENTION:  METHODS AND APPARATUS FOR SEQUENCING
;    TITLE OF INVENTION:  POLYMERS USING MASS SPECTROMETRY.
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patent Administrator - Testa, Hurwitz &
;      ADDRESSEE:  Thibeault
;      STREET:  High Street Tower, 125 High Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/844,462
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/796,598
;      FILING DATE:  07-FEB-1997
;      APPLICATION NUMBER:  US 08/446,055
;      FILING DATE:  19-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FLYNN Esq., Kerry A.
;      REGISTRATION NUMBER:  33,693
;      REFERENCE/DOCKET NUMBER:  SYP-115
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-844-462-14

  Query Match             87.7%;  Score 57;  DB 12;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


RESULT 6
US-09-025-319A-25
; Sequence 25, Application US/09025319A
;  GENERAL INFORMATION:
;    APPLICANT:  Yeaman, Michael R.
;    APPLICANT:  Shen, Alexander J.
;    TITLE OF INVENTION:  Antimicrobial Peptides And Derived Metapeptides
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FULWIDER PATTON LEE & UTECHT, LLP
;      STREET:  10877 Wilshire Blvd., Tenth Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90024
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  Hewlett Packard
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,319A
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Drucker, I. Morley
;      NAME:  Parkhurst, David G.
;      REGISTRATION NUMBER:  19,751
;      REGISTRATION NUMBER:  29,422
;      REFERENCE/DOCKET NUMBER:  REI 44454
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (310) 824-5555
;      TELEFAX:  (310) 824-9696
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    FRAGMENT TYPE:  internal fragment
;    FEATURE:
;      NAME/KEY:  RP-FBPa
;      IDENTIFICATION METHOD:  By experiment
;      OTHER INFORMATION:  microbicidal activities,
;      OTHER INFORMATION:  PMIC = -78.53; MW = 1806.90; number of charged
;      OTHER INFORMATION:  amino acids:  5
US-09-025-319A-25

  Query Match             87.7%;  Score 57;  DB 14;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


RESULT 7
US-09-525-269-25
; Sequence 25, Application US/09525269
; GENERAL INFORMATION:
;  APPLICANT: Yeaman, Michael R.
;  APPLICANT:  Shen, Alexander J.
;  TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
;  TITLE OF INVENTION:  METAPEPTIDES
;  FILE REFERENCE: 660081.415D1
;  CURRENT APPLICATION NUMBER: US/09/525,269
;  CURRENT FILING DATE:  2000-03-13
;  PRIOR APPLICATION NUMBER: US 09/025,319
;  PRIOR FILING DATE: 1998-02-18
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
;   OTHER INFORMATION: microbiocidal domains from platelet microbial
;   OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits.
US-09-525-269-25

  Query Match             87.7%;  Score 57;  DB 19;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16
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```
RESULT 8
US-09-622-561-25
; Sequence 25, Application US/09622561
; GENERAL INFORMATION:
;  APPLICANT: Yeaman, Michael R.
;  APPLICANT:  Shen, Alexander J.
;  TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
;  TITLE OF INVENTION:  METAPEPTIDES
;  FILE REFERENCE: 660081.415US
;  CURRENT APPLICATION NUMBER: US/09/622,561
;  CURRENT FILING DATE:  2000-10-06
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
;   OTHER INFORMATION: microbiocidal domains from platelet microbial
;   OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-622-561-25

  Query Match             87.7%;  Score 57;  DB 20;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 9
US-09-648-816-25
; Sequence 25, Application US/09648816
; GENERAL INFORMATION:
;  APPLICANT: Yeaman, Michael R.
;  APPLICANT:  Shen, Alexander J.
;  TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED METAPEPTIDES
;  FILE REFERENCE: 660081.415C1
;  CURRENT APPLICATION NUMBER: US/09/648,816
;  CURRENT FILING DATE:  2000-08-25
;  PRIOR APPLICATION NUMBER: US 09/622,561
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: PCT/US99/03350
;  PRIOR FILING DATE: 1999-02-17
;  PRIOR APPLICATION NUMBER: US 09/025,319
;  PRIOR FILING DATE: 1998-02-18
;  NUMBER OF SEQ ID NOS: 95
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: fragment or analogue of PMP-1 or PMP-2
US-09-648-816-25

  Query Match             87.7%;  Score 57;  DB 20;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 10
US-09-648-816A-25
; Sequence 25, Application US/09648816A
; GENERAL INFORMATION:
;  APPLICANT: Yeaman, Michael R.
;  APPLICANT:  Shen, Alexander J.
;  TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
;  TITLE OF INVENTION:  METAPEPTIDES
;  FILE REFERENCE: 660081.415C1
;  CURRENT APPLICATION NUMBER: US/09/648,816A
;  CURRENT FILING DATE:  2000-08-25
;  PRIOR APPLICATION NUMBER: US 09/622,561
;  PRIOR FILING DATE: 2000-08-18
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
;   OTHER INFORMATION: microbiocidal domains from platelet microbial
;   OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits.
US-09-648-816A-25

  Query Match             87.7%;  Score 57;  DB 20;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 11
US-09-648-816A-109
; Sequence 109, Application US/09648816A
; GENERAL INFORMATION:
;  APPLICANT: Yeaman, Michael R.
;  APPLICANT:  Shen, Alexander J.
;  TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
;  TITLE OF INVENTION:  METAPEPTIDES
;  FILE REFERENCE: 660081.415C1
;  CURRENT APPLICATION NUMBER: US/09/648,816A
;  CURRENT FILING DATE:  2000-08-25
;  PRIOR APPLICATION NUMBER: US 09/622,561
;  PRIOR FILING DATE: 2000-08-18
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
;   OTHER INFORMATION: microbiocidal domains from platelet microbial
;   OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-648-816A-109

  Query Match             87.7%;  Score 57;  DB 20;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 12
US-09-648-816B-25
; Sequence 25, Application US/09648816B
; GENERAL INFORMATION:
;  APPLICANT: Yeaman, Michael R.
;  APPLICANT:  Shen, Alexander J.
;  TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
;  TITLE OF INVENTION:  METAPEPTIDES
;  FILE REFERENCE: 660081.415C1
;  CURRENT APPLICATION NUMBER: US/09/648,816B
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;  CURRENT FILING DATE:  2000-08-25
;  PRIOR APPLICATION NUMBER: US 09/622,561
;  PRIOR FILING DATE: 2000-08-18
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
;   OTHER INFORMATION: microbiocidal domains from platelet microbial
;   OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits.
US-09-648-816B-25

  Query Match             87.7%;  Score 57;  DB 20;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


RESULT 13
US-09-657-276-1135
; Sequence 1135, Application US/09657276
; GENERAL INFORMATION:
;  APPLICANT:  Conjuchem, Inc.
;  APPLICANT:  Bridon, Dominique
;  APPLICANT:  Ezrin, Alan
;  APPLICANT:  Milner, Peter
;  APPLICANT:  Holmes, Darren
;  APPLICANT:  Thibaudeau, Karen
;  TITLE OF INVENTION:  PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;  TITLE OF INVENTION:  PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;  TITLE OF INVENTION:  COMPONENTS
;  FILE REFERENCE:  2110
;  CURRENT APPLICATION NUMBER: US/09/657,276
;  CURRENT FILING DATE:  2000-09-07
;  PRIOR APPLICATION NUMBER:  60/134,406
;  PRIOR FILING DATE:  1999-05-17
;  PRIOR APPLICATION NUMBER:  60/153,406
;  PRIOR FILING DATE:  1999-09-10
;  PRIOR APPLICATION NUMBER:  60/159,783
;  PRIOR FILING DATE:  1999-10-18
;  NUMBER OF SEQ ID NOS:  1617
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1135
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-657-276-1135

  Query Match             87.7%;  Score 57;  DB 20;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


RESULT 14
US-09-826-290-352
; Sequence 352, Application US/09826290
; GENERAL INFORMATION:
;  APPLICANT: Durham, L.Kathryn
;  APPLICANT:  Friedman, David L.
;  APPLICANT:  Herath, Herath Mudiyanselage Athula Chandrasiri
;  APPLICANT:  Kimmel, Lida H.
;  APPLICANT:  Parekh, Rajesh Bhikhu
;  APPLICANT:  Potter, David M.
;  APPLICANT:  Rohlff, Christian
;  APPLICANT:  Silber, B. Michael
;  APPLICANT:  Stiger, Thomas R.
;  APPLICANT:  Sunderland, P. Trey
;  APPLICANT:  Townsend, Robert Reid
;  APPLICANT:  White, Frost
;  APPLICANT:  Williams, Stephen A.
;  TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
;  TITLE OF INVENTION:  Uses Therefor, Including Diagnosis and Treatment of
;  TITLE OF INVENTION:  Alzheimer's Disease
;  FILE REFERENCE: 2572-1-001 N2
;  CURRENT APPLICATION NUMBER: US/09/826,290
;  CURRENT FILING DATE:  2001-04-30
;  PRIOR APPLICATION NUMBER: US 60/194,504
;  PRIOR FILING DATE: 2000-04-03
;  PRIOR APPLICATION NUMBER: US 60/253,647
;  PRIOR FILING DATE: 2000-11-28
;  NUMBER OF SEQ ID NOS: 492
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 352
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: homo sapien
US-09-826-290-352

  Query Match             87.7%;  Score 57;  DB 22;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


RESULT 15
US-09-845-765-1
; Sequence 1, Application US/09845765
; GENERAL INFORMATION:
;  APPLICANT: Jackowski, George
;  TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
;  TITLE OF INVENTION:  OF 1518 DALTONS
;  FILE REFERENCE: 2132.036
;  CURRENT APPLICATION NUMBER: US/09/845,765
;  CURRENT FILING DATE:  2001-04-30
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-845-765-1

  Query Match             87.7%;  Score 57;  DB 22;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


Search completed: February 10, 2003, 16:13:47
Job time : 356 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 16:01:12 ; Search time 61 Seconds
(without alignments)
17.726 Million cell updates/sec

Title: US-09-845-729-1
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 420310 seqs, 83175323 residues

Total number of hits satisfying chosen parameters: 420310

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	65	100.0	13	5	US-09-845-729-1	Sequence 1, Appli
2	57	87.7	16	6	US-10-325-162-1	Sequence 1, Appli
3	57	87.7	70	5	US-09-724-676-71849	Sequence 71849, A
4	57	87.7	70	5	US-09-724-676A-71849	Sequence 71849, A
5	57	87.7	93	5	US-09-724-676-71847	Sequence 71847, A
6	57	87.7	93	5	US-09-724-676A-71847	Sequence 71847, A
7	57	87.7	388	6	US-10-236-392-34	Sequence 34, Appl
8	57	87.7	481	6	US-10-236-392-36	Sequence 36, Appl
9	57	87.7	644	1	PCT-US02-37760-5	Sequence 5, Appli
10	57	87.7	644	6	US-10-236-392-32	Sequence 32, Appl
11	57	87.7	866	1	PCT-US02-37760-6	Sequence 6, Appli
12	57	87.7	866	5	US-09-949-002-302	Sequence 302, App
13	57	87.7	875	5	US-09-949-002-455	Sequence 455, App
14	46	70.8	17	6	US-10-293-580-45	Sequence 45, Appl
15	40	61.5	489	6	US-10-310-154-381	Sequence 381, App
16	39	60.0	286	5	US-09-950-084-5126	Sequence 5126, Ap
17	38	58.5	115	5	US-09-513-999C-5898	Sequence 5898, Ap
18	38	58.5	320	5	US-09-724-676-62455	Sequence 62455, A
19	38	58.5	320	5	US-09-724-676A-62455	Sequence 62455, A
20	38	58.5	325	5	US-09-724-676-62456	Sequence 62456, A
21	38	58.5	325	5	US-09-724-676A-62456	Sequence 62456, A
22	38	58.5	608	1	PCT-US02-35563-27	Sequence 27, Appl
23	38	58.5	611	6	US-10-223-089-340	Sequence 340, App
24	38	58.5	671	5	US-09-724-676-62453	Sequence 62453, A
25	38	58.5	671	5	US-09-724-676A-62453	Sequence 62453, A
26	38	58.5	676	5	US-09-724-676-62454	Sequence 62454, A
27	38	58.5	676	5	US-09-724-676A-62454	Sequence 62454, A
28	38	58.5	722	5	US-09-724-676-62452	Sequence 62452, A
29	38	58.5	722	5	US-09-724-676A-62452	Sequence 62452, A
30	37	56.9	381	6	US-10-099-056-1416	Sequence 1416, Ap
31	36	55.4	11	6	US-10-212-499-39	Sequence 39, Appl
32	36	55.4	175	6	US-10-264-237-1928	Sequence 1928, Ap
33	36	55.4	311	5	US-09-724-676-75821	Sequence 75821, A
34	36	55.4	311	5	US-09-724-676A-75821	Sequence 75821, A
35	36	55.4	426	6	US-10-203-138A-13561	Sequence 13561, A
36	36	55.4	500	6	US-10-288-798-4	Sequence 4, Appli
37	36	55.4	611	7	US-60-428-082-19	Sequence 19, Appl
38	36	55.4	1268	6	US-10-276-774-2166	Sequence 2166, Ap
39	36	55.4	1472	5	US-09-724-676-57022	Sequence 57022, A
40	36	55.4	1472	5	US-09-724-676A-57022	Sequence 57022, A
41	36	55.4	1493	5	US-09-724-676-57021	Sequence 57021, A
42	36	55.4	1493	5	US-09-724-676A-57021	Sequence 57021, A
43	36	55.4	1583	1	PCT-US02-32727-15149	Sequence 15149, A
44	36	55.4	1583	6	US-10-057-498-15149	Sequence 15149, A
45	36	55.4	1783	6	US-10-275-140-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-845-729-1
; Sequence 1, Application US/09845729
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 1350 DALTONS
; FILE REFERENCE: 2132.031
; CURRENT APPLICATION NUMBER: US/09/845,729
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-729-1

Query Match 100.0%; Score 65; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SESDFLAEGGGVR 13
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Db 1 SESDFLAEGGGVR 13

RESULT 2
US-10-325-162-1
; Sequence 1, Application US/10325162
; GENERAL INFORMATION:
; APPLICANT: Kupchak, Peter
; APPLICANT: Marshall, John
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Method of Confirming the Presence of Myocardial Infarction
; FILE REFERENCE: 2132.132
; CURRENT APPLICATION NUMBER: US/10/325,162
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-325-162-1

Query Match 87.7%; Score 57; DB 6; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0085;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 3
US-09-724-676-71849
; Sequence 71849, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71849
;   LENGTH: 70
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-676-71849

  Query Match             87.7%;  Score 57;  DB 5;  Length 70;
  Best Local Similarity   91.7%;  Pred. No. 0.034;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db     24 EGDFLAEGGGVR 35


RESULT 4
US-09-724-676A-71849
; Sequence 71849, Application US/09724676A
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71849
;   LENGTH: 70
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-676A-71849

  Query Match             87.7%;  Score 57;  DB 5;  Length 70;
  Best Local Similarity   91.7%;  Pred. No. 0.034;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db     24 EGDFLAEGGGVR 35


RESULT 5
US-09-724-676-71847
; Sequence 71847, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71847
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-676-71847

  Query Match             87.7%;  Score 57;  DB 5;  Length 93;
  Best Local Similarity   91.7%;  Pred. No. 0.045;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db     42 EGDFLAEGGGVR 53


RESULT 6
US-09-724-676A-71847
; Sequence 71847, Application US/09724676A
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71847
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-676A-71847

  Query Match             87.7%;  Score 57;  DB 5;  Length 93;
  Best Local Similarity   91.7%;  Pred. No. 0.045;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db     42 EGDFLAEGGGVR 53


RESULT 7
US-10-236-392-34
; Sequence 34, Application US/10236392
; GENERAL INFORMATION:
;  APPLICANT: Anderson, David W
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Burgess, Catherine, E
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Chapoval, Andrei
;  APPLICANT:  Crabtree, Julie
;  APPLICANT:  Edinger, Shlomit, R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Gusev, Vladamir
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  LaRochelle, William J
;  APPLICANT:  Li, Li
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol A
;  APPLICANT:  Peyman, John A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Reiger, Daniel K
;  APPLICANT:  Rothenberg, Mark E
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-442A
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; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 34
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-34

Query Match 87.7%; Score 57; DB 6; Length 388;
Best Local Similarity 91.7%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db      24 EGDFLAEGGGVR 35
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RESULT 8
US-10-236-392-36
; Sequence 36, Application US/10236392
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladamir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 36
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-36

Query Match 87.7%; Score 57; DB 6; Length 481;
Best Local Similarity 91.7%; Pred. No. 0.21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db      24 EGDFLAEGGGVR 35
```

RESULT 9
PCT-US02-37760-5
; Sequence 5, Application PC/TUS0237760
; GENERAL INFORMATION:
; APPLICANT: GENVEC, INC.
; APPLICANT: KESSLER, PAUL D
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: ANGIOPOIETIN RELATED FACTORS
; FILE REFERENCE: 220091
; CURRENT APPLICATION NUMBER: PCT/US02/37760
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/334488
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-37760-5

Query Match 87.7%; Score 57; DB 1; Length 644;
Best Local Similarity 91.7%; Pred. No. 0.28;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db      24 EGDFLAEGGGVR 35
```

```
RESULT 10
US-10-236-392-32
; Sequence 32, Application US/10236392
; GENERAL INFORMATION:
;  APPLICANT: Anderson, David W
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Burgess, Catherine, E
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Chapoval, Andrei
;  APPLICANT:  Crabtree, Julie
;  APPLICANT:  Edinger, Shlomit, R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Gusev, Vladamir
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  LaRochelle, William J
;  APPLICANT:  Li, Li
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol A
;  APPLICANT:  Peyman, John A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Reiger, Daniel K
;  APPLICANT:  Rothenberg, Mark E
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-442A
;  CURRENT APPLICATION NUMBER: US/10/236,392
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US09/540,763
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US60/390,155
;  PRIOR FILING DATE: 2002-06-19
;  PRIOR APPLICATION NUMBER: US09/635,949
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US60/318,765
;  PRIOR FILING DATE: 2001-09-12
;  PRIOR APPLICATION NUMBER: US60/357,303
;  PRIOR FILING DATE: 2002-02-15
;  PRIOR APPLICATION NUMBER: US60/367,753
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: US60/369,479
;  PRIOR FILING DATE: 2002-04-02
;  PRIOR APPLICATION NUMBER: US09/659,634
;  PRIOR FILING DATE: 2000-09-12
;  PRIOR APPLICATION NUMBER: US60/318,120
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US60/318,130
;  PRIOR FILING DATE: 2001-09-07
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 794
;  SOFTWARE: Custom
; SEQ ID NO 32
;   LENGTH: 644
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-236-392-32

  Query Match             87.7%;  Score 57;  DB 6;  Length 644;
  Best Local Similarity   91.7%;  Pred. No. 0.28;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db      24 EGDFLAEGGGVR 35


RESULT 11
PCT-US02-37760-6
; Sequence 6, Application PC/TUS0237760
; GENERAL INFORMATION:
;  APPLICANT: GENVEC, INC.
;  APPLICANT:  KESSLER, PAUL D
;  APPLICANT:  KOVESDI, IMRE
;  TITLE OF INVENTION: ANGIOPOIETIN RELATED FACTORS
;  FILE REFERENCE: 220091
;  CURRENT APPLICATION NUMBER: PCT/US02/37760
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 60/334488
;  PRIOR FILING DATE: 2001-11-30
;  NUMBER OF SEQ ID NOS: 174
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 866
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-37760-6

  Query Match             87.7%;  Score 57;  DB 1;  Length 866;
  Best Local Similarity   91.7%;  Pred. No. 0.38;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db      24 EGDFLAEGGGVR 35


RESULT 12
US-09-949-002-302
; Sequence 302, Application US/09949002
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000790
;  CURRENT APPLICATION NUMBER: US/09/949,002
;  CURRENT FILING DATE:  2000-01-28
;  PRIOR APPLICATION NUMBER: 60/231,401
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 10823
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 302
;   LENGTH: 866
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-002-302

  Query Match             87.7%;  Score 57;  DB 5;  Length 866;
  Best Local Similarity   91.7%;  Pred. No. 0.38;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db      24 EGDFLAEGGGVR 35


RESULT 13
US-09-949-002-455
; Sequence 455, Application US/09949002
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000790
;  CURRENT APPLICATION NUMBER: US/09/949,002
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;  CURRENT FILING DATE:  2000-01-28
;  PRIOR APPLICATION NUMBER: 60/231,401
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 10823
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 455
;   LENGTH: 875
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-002-455

  Query Match             87.7%;  Score 57;  DB 5;  Length 875;
  Best Local Similarity   91.7%;  Pred. No. 0.38;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db     33 EGDFLAEGGGVR 44


RESULT 14
US-10-293-580-45
; Sequence 45, Application US/10293580
; GENERAL INFORMATION:
;  APPLICANT: Aurora Biosciences Corporation
;  APPLICANT:  Cubitt, Andrew B.
;  TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
;  FILE REFERENCE: AURO1270 (08366/031001)
;  CURRENT APPLICATION NUMBER: US/10/293,580
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: US/09/129,192
;  PRIOR FILING DATE: 1998-07-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: thrombin
US-10-293-580-45

  Query Match             70.8%;  Score 46;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.49;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 FLAEGGGVR 13
          |||||||||
Db      1 FLAEGGGVR 9


RESULT 15
US-10-310-154-381
; Sequence 381, Application US/10310154
; GENERAL INFORMATION:
;  APPLICANT: Edgerton, Michael D
;  APPLICANT:  Chomet, Paul S.
;  APPLICANT:  Adams, Thomas H
;  APPLICANT:  Ruff, Thomas G.
;  APPLICANT:  Agarwal, Ameeta K.
;  APPLICANT:  Ahrens, Jeffrey E.
;  APPLICANT:  Ball, James A.
;  APPLICANT:  Banu, G.
;  APPLICANT:  Bell, Erin
;  APPLICANT:  Boddupalli, Raghava
;  APPLICANT:  Deikman, Jill
;  APPLICANT:  Deng, Molian
;  APPLICANT:  Dong, Jinzhuo
;  APPLICANT:  Duff, Stephen M.
;  APPLICANT:  Galligan, Meghan M.
;  APPLICANT:  Hinchey, Brenda S.
;  APPLICANT:  Huang, Shihshieh
;  APPLICANT:  Johnson, G. Richard
;  APPLICANT:  Jung, Vincent
;  APPLICANT:  Kretzmer, Keith A
;  APPLICANT:  Laccetti, Lucille B.
;  APPLICANT:  Lai, Chao-Qiang
;  APPLICANT:  Lee, Gary
;  APPLICANT:  Lin, Jie-Yi
;  APPLICANT:  Liu, Jingdong
;  APPLICANT:  Lu, Bin
;  APPLICANT:  Luethy, Michael M.
;  APPLICANT:  Lund, Adrian
;  APPLICANT:  Madson, Linda L.
;  APPLICANT:  Malloy, Kathleen A.
;  APPLICANT:  McKiel, Christine L.
;  APPLICANT:  Miller, Philip W.
;  APPLICANT:  Padmavathi, Manchikanti
;  APPLICANT:  Parnell, Laurence D.
;  APPLICANT:  Start, William G.
;  APPLICANT:  Tennesen, Dan
;  APPLICANT:  Vidya, K.R.
;  APPLICANT:  Wang, Haiyun
;  APPLICANT:  Xin, Zhanguo
;  APPLICANT:  Xu, Nanfei
;  APPLICANT:  Yang, Chunzhi
;  APPLICANT:  Zeng, Xiaoping
;  APPLICANT:  Zhang, Qiang
;  APPLICANT:  Zhao, Yajuan
;  APPLICANT:  Zhou, Li
;  TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
;  FILE REFERENCE: 38-15(52796)B
;  CURRENT APPLICATION NUMBER: US/10/310,154
;  CURRENT FILING DATE:  2002-12-04
;  PRIOR APPLICATION NUMBER: 60/337,358
;  PRIOR FILING DATE: 2001-12-04
;  NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 381
;   LENGTH: 489
;   TYPE: PRT
;   ORGANISM: Zea mays
US-10-310-154-381

  Query Match             61.5%;  Score 40;  DB 6;  Length 489;
  Best Local Similarity   53.8%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 SESDFLAEGGGVR 13
            :  ||:| |||:|
Db    419 TSKDFMAFGGGLR 431


Search completed: February 10, 2003, 16:14:54
Job time : 61 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 15:55:46 ; Search time 82 Seconds
(without alignments)
21.125 Million cell updates/sec

Title: US-09-845-729-1
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
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9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
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14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
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17: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	87.7	16	17	AAR96194	Fibrinogen epitope
2	57	87.7	16	18	AAW04619	Fibrinopeptide A p
3	57	87.7	16	20	AAY57487	Antimicrobial pept
4	57	87.7	16	22	ABB56219	Vascular dementia-
5	57	87.7	16	22	ABB52337	Human API-118 tryp
6	57	87.7	16	22	AAB91959	Fibronectin fragme
7	57	87.7	17	17	AAR96184	Fibrinogen epitope
8	57	87.7	17	22	AAB91960	Fibronectin fragme
9	57	87.7	18	17	AAR96193	Fibrinogen epitope
10	57	87.7	19	17	AAR96192	Fibrinogen epitope
11	57	87.7	20	17	AAR96191	Fibrinogen epitope
12	57	87.7	20	20	AAY57488	Antimicrobial pept
13	57	87.7	21	17	AAR96183	Fibrinogen epitope
14	57	87.7	22	10	AAP90276	Antigen probe for
15	57	87.7	22	17	AAR96182	Fibrinogen epitope
16	57	87.7	22	17	AAR96190	Fibrinogen epitope
17	57	87.7	24	23	AAO21112	Anti-angiogenic al
18	57	87.7	24	23	AAO21113	Anti-angiogenic al
19	57	87.7	24	23	AAO21114	Anti-angiogenic al
20	57	87.7	24	23	AAO21115	Anti-angiogenic al
21	57	87.7	24	23	AAO21118	Anti-angiogenic al
22	57	87.7	24	23	AAO21119	Anti-angiogenic al
23	57	87.7	24	23	AAO21120	Anti-angiogenic al
24	57	87.7	25	23	AAG79318	Lupus peptide, CI-
25	57	87.7	25	23	AAM51100	Peptide used in pu
26	57	87.7	78	23	AAO21122	Fibrinogen E alpha
27	57	87.7	78	23	AAO14005	Human fibrinogen E
28	57	87.7	360	21	AAB54135	Human pancreatic c
29	57	87.7	643	15	AAR60020	Fibronectin. Homo
30	57	87.7	644	16	AAR82244	Human fibrinogen A
31	57	87.7	847	21	AAY82891	AlphaE subunit of
32	52	80.0	15	10	AAP91735	Antigenic C-termin
33	52	80.0	15	17	AAR96155	Fibrinogen antigen
34	52	80.0	24	23	AAO21116	Anti-angiogenic al
35	52	80.0	28	12	AAR11166	Hirulog-33. Synth
36	50	76.9	24	23	AAO21117	Anti-angiogenic al
37	50	76.9	24	23	AAO21121	Anti-angiogenic al
38	50	76.9	140	21	AAY96839	PCpB-DFIAEGGGVR-hP
39	46	70.8	17	23	AAE19125	Thrombin peptide.
40	46	70.8	24	19	AAW64264	Murine 34-, 40 and
41	45	69.2	24	23	AAO21111	Anti-angiogenic al
42	43	66.2	14	22	AAB50472	Fibrinogen-derived
43	42	64.6	98	21	AAB14308	Human secreted pro
44	42	64.6	98	22	AAB85230	Human secreted pro
45	40	61.5	13	17	AAR96185	Fibrinogen epitope

ALIGNMENTS

RESULT 1
AAR96194
ID AAR96194 standard; peptide; 16 AA.
XX
AC AAR96194;
XX
DT 19-DEC-1996 (first entry)
XX
DE Fibrinogen epitope probe, represents alpha chain residues 1-16.
XX
KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
KW sputum; broncheoalveolar lavage fluid; assay; inhibitor; arthritis;
KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
KW chronic obstructive pulmonary disease; myelogenous leukaemia;
KW infantile respiratory distress syndrome; gout;
KW adult respiratory distress syndrome.
XX
OS Homo sapiens.
XX
PN WO9614580-A1.
XX
PD 17-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US13794.
XX
PR 06-JUN-1995; 95US-0469141.
PR 07-NOV-1994; 94US-0335524.
XX
PA (MERI) MERCK & CO INC.
XX
PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;
XX

DR WPI; 1996-251888/25.
XX
PT New isolated fibrinogen derived cleavage products - used for
PT detection of leukocyte elastase activity in disease diagnosis and
PT for evaluating elastase inhibitors
XX
PS Example 5; Page 42; 109pp; English.
XX
CC The sequences given in AAR96182-94 represent antigenic probes derived
CC from the first 21 amino acids of human fibrinogen. These probes are
CC used to determine antibody titre against other fibrinogen cleavage
CC products. The monospecific antibodies may be used to assay for the
CC formation of complimentary cleavage product antigens or epitopes in
CC whole blood or other body fluids, peritoneal fluid, sputum or
CC broncheoalveolar lavage fluid. The assay for cleavage products is
CC dependent upon the presence of HLE in the sample. This assay can also
CC be used for the evaluation of HLE inhibitors. The antibodies may be
CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
CC pulmonary disease, bronchiectasis, adult or infantile respiratory
CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 17; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.004;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 2
AAW04619
ID AAW04619 standard; peptide; 16 AA.
XX
AC AAW04619;
XX
DT 13-AUG-1997 (first entry)
XX
DE Fibrinopeptide A peptide for mass spectrometry analysis.
XX
KW Mass spectrometry; polymer analysis; biopolymer analysis.
XX
OS Synthetic.
XX
PN WO9636986-A1.
XX
PD 21-NOV-1996.
XX
PF 17-MAY-1996; 96WO-US07146.
XX
PR 19-MAY-1995; 95US-0447175.
PR 19-MAY-1995; 95US-0446055.
XX
PA (PERS-) PERSEPTIVE BIOSYSTEMS INC.
XX
PI Patterson DH, Tarr GE;
XX
DR WPI; 1997-012308/01.
XX
PT Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins,
PT etc. - by obtaining mass to charge ratios of polymer fragments,
PT pref. using mass spectrometer, and performing statistical analysis
XX
PS Example 2; Page 32; 86pp; English.
XX
CC A method of obtaining sequence information about a polymer (e.g. DNA,
CC RNA, peptide nucleic acids, proteins, peptides and carbohydrates)
CC comprising monomers of known mass has been claimed. The present
CC sequence represents a fibrinopeptide A peptide, and was used as
CC an example as a digestion before analysis by mass spectrometry,
CC using this novel on-plate strategy. Total sequence information
CC from a nine well digestion can be represented in a single digestion or
CC it is often derived from two or more wells. The methods, apparatus and
CC kit (claimed) can be used for the analysis of polymers, particularly
CC biopolymers, e.g. DNA, RNA, peptide nucleic acids, proteins, peptides
CC and carbohydrates. It provides a rapid, automated and cost effective
CC sequencing of polymers, with a statistical certainty.
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 18; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.004;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 3
AAY57487
ID AAY57487 standard; Peptide; 16 AA.
XX
AC AAY57487;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide CS-FBP-alpha SEQ ID NO:25.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US03350.
XX
PR 18-FEB-1998; 98US-0025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi -
XX
PS Disclosure; Page 120; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZBXBXB and its derivatives
CC selected from XZBBZBXBXB, BXZXB, BXZXZXB, XBBXZXBBX and BBXZBBXZ; and
CC (b) a second peptide template XBBXX and their derivatives selected from
CC the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and
CC XBBZXXBBXXZBBX; where B = at least one positively charged amino acid;
CC X = at least one non-polar hydrophobic amino acid; Z = at least one
CC aromatic amino acid, and where B, X and Z may be separated by one or
CC more other amino acids. The peptides can be used to treat bacterial and
CC fungal infections. The peptides also increase the antimicrobial activity
CC of neutrophils. The peptides overall effect cellular disruption and
CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 20; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.004;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 4
ABB56219
ID ABB56219 standard; Peptide; 16 AA.
XX
AC ABB56219;
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 419.
XX
KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KW diagnosis; prognosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB01106.
XX
PR 15-MAR-2000; 2000GB-0006285.
PR 24-NOV-2000; 2000GB-0028734.
PR 28-NOV-2000; 2000US-0724391.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlff C;
XX
DR WPI; 2001-557937/62.
XX
PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy,
PT comprises analysing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD -
XX
PS Claim 6; Page 39; 151pp; English.
XX
CC The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for
CC monitoring the effect of therapy administered to a subject having VD.
CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
CC useful for the treatment of VD and for gene therapy.
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 22; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.004;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 5
ABB52337
ID ABB52337 standard; Peptide; 16 AA.
XX
AC ABB52337;
XX
DT 08-FEB-2002 (first entry)
XX
DE Human API-118 tryptic digest peptide #2.
XX
KW Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX
OS Homo sapiens.
XX
PN WO200175454-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US10908.
XX
PR 03-APR-2000; 2000US-194504P.
PR 28-NOV-2000; 2000US-253647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ) PFIZER INC.
XX
PI Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;
PI Potter DM, Rohlff C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
DR WPI; 2001-639384/73.
XX
PT Screening for Alzheimer's disease in a mammal, by making
PT two-dimensional array of a feature whose relative abundance correlates
PT with disease, and comparing with abundance of the feature in samples of
PT healthy persons -
XX
PS Example; Page 33; 162pp; English.
XX
CC The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection
CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
CC serum or plasma. The abundance of the AFs and APIs is then
CC normalised to an Expression Reference Protein Isoform (ERPI) in
CC order to determine whether a patient is suffering from, or has
CC a predisposition to, Alzheimer's Disease. The relative abundance of
CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
CC The present sequence is a peptide produced from an API by proteolysis.
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 22; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.004;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 6
AAB91959
ID AAB91959 standard; Peptide; 16 AA.
XX
AC AAB91959;
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1135.

XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
PS Disclosure; Page 567; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 22; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.004;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 7
AAR96184
ID AAR96184 standard; peptide; 17 AA.
XX
AC AAR96184;
XX
DT 19-DEC-1996 (first entry)
XX
DE Fibrinogen epitope probe, represents alpha chain residues 5-21.
XX
KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
KW sputum; broncheoalveolar lavage fluid; assay; inhibitor; arthritis;
KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
KW chronic obstructive pulmonary disease; myelogenous leukaemia;
KW infantile respiratory distress syndrome; gout;
KW adult respiratory distress syndrome.
XX
OS Homo sapiens.
XX
PN WO9614580-A1.
XX
PD 17-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US13794.
XX
PR 06-JUN-1995; 95US-0469141.
PR 07-NOV-1994; 94US-0335524.
XX
PA (MERI) MERCK & CO INC.
XX
PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;
XX
DR WPI; 1996-251888/25.
XX
PT New isolated fibrinogen derived cleavage products - used for
PT detection of leukocyte elastase activity in disease diagnosis and
PT for evaluating elastase inhibitors
XX
PS Example 5; Page 41; 109pp; English.
XX
CC The sequences given in AAR96182-94 represent antigenic probes derived
CC from the first 21 amino acids of human fibrinogen. These probes are
CC used to determine antibody titre against other fibrinogen cleavage
CC products. The monospecific antibodies may be used to assay for the
CC formation of complimentary cleavage product antigens or epitopes in
CC whole blood or other body fluids, peritoneal fluid, sputum or
CC broncheoalveolar lavage fluid. The assay for cleavage products is
CC dependent upon the presence of HLE in the sample. This assay can also
CC be used for the evaluation of HLE inhibitors. The antibodies may be
CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
CC pulmonary disease, bronchiectasis, adult or infantile respiratory
CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.
XX
SQ Sequence 17 AA;

Query Match 87.7%; Score 57; DB 17; Length 17;
Best Local Similarity 91.7%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 1 EGDFLAEGGGVR 12

RESULT 8
AAB91960
ID AAB91960 standard; Peptide; 17 AA.
XX
AC AAB91960;
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1136.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX

PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
PS Disclosure; Page 567; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 17 AA;

Query Match 87.7%; Score 57; DB 22; Length 17;
Best Local Similarity 91.7%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 6 EGDFLAEGGGVR 17

RESULT 9
AAR96193
ID AAR96193 standard; peptide; 18 AA.
XX
AC AAR96193;
XX
DT 19-DEC-1996 (first entry)
XX
DE Fibrinogen epitope probe, represents alpha chain residues 1-18.
XX
KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
KW sputum; broncheoalveolar lavage fluid; assay; inhibitor; arthritis;
KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
KW chronic obstructive pulmonary disease; myelogenous leukaemia;
KW infantile respiratory distress syndrome; gout;
KW adult respiratory distress syndrome.
XX
OS Homo sapiens.
XX
PN WO9614580-A1.
XX
PD 17-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US13794.
XX
PR 06-JUN-1995; 95US-0469141.
PR 07-NOV-1994; 94US-0335524.
XX
PA (MERI) MERCK & CO INC.
XX
PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;
XX
DR WPI; 1996-251888/25.
XX
PT New isolated fibrinogen derived cleavage products - used for
PT detection of leukocyte elastase activity in disease diagnosis and
PT for evaluating elastase inhibitors
XX
PS Example 5; Page 42; 109pp; English.
XX
CC The sequences given in AAR96182-94 represent antigenic probes derived
CC from the first 21 amino acids of human fibrinogen. These probes are
CC used to determine antibody titre against other fibrinogen cleavage
CC products. The monospecific antibodies may be used to assay for the
CC formation of complimentary cleavage product antigens or epitopes in
CC whole blood or other body fluids, peritoneal fluid, sputum or
CC broncheoalveolar lavage fluid. The assay for cleavage products is
CC dependent upon the presence of HLE in the sample. This assay can also
CC be used for the evaluation of HLE inhibitors. The antibodies may be
CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
CC pulmonary disease, bronchiectasis, adult or infantile respiratory
CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.
XX
SQ Sequence 18 AA;

Query Match 87.7%; Score 57; DB 17; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.0045;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 10
AAR96192
ID AAR96192 standard; peptide; 19 AA.
XX
AC AAR96192;
XX
DT 19-DEC-1996 (first entry)
XX
DE Fibrinogen epitope probe, represents alpha chain residues 1-19.
XX
KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
KW sputum; broncheoalveolar lavage fluid; assay; inhibitor; arthritis;
KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
KW chronic obstructive pulmonary disease; myelogenous leukaemia;
KW infantile respiratory distress syndrome; gout;
KW adult respiratory distress syndrome.
XX
OS Homo sapiens.
XX
PN WO9614580-A1.
XX
PD 17-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US13794.
XX
PR 06-JUN-1995; 95US-0469141.
PR 07-NOV-1994; 94US-0335524.
XX
PA (MERI) MERCK & CO INC.
XX
PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;
XX

DR WPI; 1996-251888/25.
XX
PT New isolated fibrinogen derived cleavage products - used for
PT detection of leukocyte elastase activity in disease diagnosis and
PT for evaluating elastase inhibitors
XX
PS Example 5; Page 42; 109pp; English.
XX
CC The sequences given in AAR96182-94 represent antigenic probes derived
CC from the first 21 amino acids of human fibrinogen. These probes are
CC used to determine antibody titre against other fibrinogen cleavage
CC products. The monospecific antibodies may be used to assay for the
CC formation of complimentary cleavage product antigens or epitopes in
CC whole blood or other body fluids, peritoneal fluid, sputum or
CC broncheoalveolar lavage fluid. The assay for cleavage products is
CC dependent upon the presence of HLE in the sample. This assay can also
CC be used for the evaluation of HLE inhibitors. The antibodies may be
CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
CC pulmonary disease, bronchiectasis, adult or infantile respiratory
CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.
XX
SQ Sequence 19 AA;

Query Match 87.7%; Score 57; DB 17; Length 19;
Best Local Similarity 91.7%; Pred. No. 0.0048;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16
```

RESULT 11
AAR96191
ID AAR96191 standard; peptide; 20 AA.
XX
AC AAR96191;
XX
DT 19-DEC-1996 (first entry)
XX
DE Fibrinogen epitope probe, represents alpha chain residues 1-20.
XX
KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
KW sputum; broncheoalveolar lavage fluid; assay; inhibitor; arthritis;
KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
KW chronic obstructive pulmonary disease; myelogenous leukaemia;
KW infantile respiratory distress syndrome; gout;
KW adult respiratory distress syndrome.
XX
OS Homo sapiens.
XX
PN WO9614580-A1.
XX
PD 17-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US13794.
XX
PR 06-JUN-1995; 95US-0469141.
PR 07-NOV-1994; 94US-0335524.
XX
PA (MERI) MERCK & CO INC.
XX
PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;
XX
DR WPI; 1996-251888/25.
XX
PT New isolated fibrinogen derived cleavage products - used for
PT detection of leukocyte elastase activity in disease diagnosis and
PT for evaluating elastase inhibitors
XX
PS Example 5; Page 42; 109pp; English.
XX
CC The sequences given in AAR96182-94 represent antigenic probes derived
CC from the first 21 amino acids of human fibrinogen. These probes are
CC used to determine antibody titre against other fibrinogen cleavage
CC products. The monospecific antibodies may be used to assay for the
CC formation of complimentary cleavage product antigens or epitopes in
CC whole blood or other body fluids, peritoneal fluid, sputum or
CC broncheoalveolar lavage fluid. The assay for cleavage products is
CC dependent upon the presence of HLE in the sample. This assay can also
CC be used for the evaluation of HLE inhibitors. The antibodies may be
CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
CC pulmonary disease, bronchiectasis, adult or infantile respiratory
CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.
XX
SQ Sequence 20 AA;

Query Match 87.7%; Score 57; DB 17; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.0051;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16
```

RESULT 12
AAY57488
ID AAY57488 standard; Peptide; 20 AA.
XX
AC AAY57488;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide CS-FBP-alpha-TET SEQ ID NO:26.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US03350.
XX
PR 18-FEB-1998; 98US-0025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi -
XX
PS Disclosure; Page 120; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZBXBXB and its derivatives
CC selected from XZBBZBXBXB, BXZXB, BXZXZXB, XBBXZXBBX and BBXZBBXZ; and
CC (b) a second peptide template XBBXX and their derivatives selected from
CC the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and
CC XBBZXXBBXXZBBX; where B = at least one positively charged amino acid;
CC X = at least one non-polar hydrophobic amino acid; Z = at least one
CC aromatic amino acid, and where B, X and Z may be separated by one or
CC more other amino acids. The peptides can be used to treat bacterial and

```
CC   fungal infections. The peptides also increase the antimicrobial activity
CC   of neutrophils. The peptides overall effect cellular disruption and
CC   rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
CC   sequences used in the exemplification of the present invention.
XX
SQ   Sequence   20 AA;

  Query Match             87.7%;  Score 57;  DB 20;  Length 20;
  Best Local Similarity   91.7%;  Pred. No. 0.0051;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 13
AAR96183
ID   AAR96183 standard; peptide; 21 AA.
XX
AC   AAR96183;
XX
DT   19-DEC-1996  (first entry)
XX
DE   Fibrinogen epitope probe, represents alpha chain residues 1-21.
XX
KW   Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
KW   monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
KW   sputum; broncheoalveolar lavage fluid; assay; inhibitor; arthritis;
KW   pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
KW   chronic obstructive pulmonary disease; myelogenous leukaemia;
KW   infantile respiratory distress syndrome; gout;
KW   adult respiratory distress syndrome.
XX
OS   Homo sapiens.
XX
PN   WO9614580-A1.
XX
PD   17-MAY-1996.
XX
PF   03-NOV-1995;   95WO-US13794.
XX
PR   06-JUN-1995;   95US-0469141.
PR   07-NOV-1994;   94US-0335524.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Boger JS,  Dahlgren ME,  Davies DTP,  Humes JL,  Mumford RA;
XX
DR   WPI; 1996-251888/25.
XX
PT   New isolated fibrinogen derived cleavage products - used for
PT   detection of leukocyte elastase activity in disease diagnosis and
PT   for evaluating elastase inhibitors
XX
PS   Example 5; Page 41; 109pp; English.
XX
CC   The sequences given in AAR96182-94 represent antigenic probes derived
CC   from the first 21 amino acids of human fibrinogen.  These probes are
CC   used to determine antibody titre against other fibrinogen cleavage
CC   products.  The monospecific antibodies may be used to assay for the
CC   formation of complimentary cleavage product antigens or epitopes in
CC   whole blood or other body fluids, peritoneal fluid, sputum or
CC   broncheoalveolar lavage fluid.  The assay for cleavage products is
CC   dependent upon the presence of HLE in the sample.  This assay can also
CC   be used for the evaluation of HLE inhibitors.  The antibodies may be
CC   used to diagnose and monitor diseases such as arthritis, gout, pulmonary
CC   emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
CC   pulmonary disease, bronchiectasis, adult or infantile respiratory
CC   distress syndrome and myelogenous leukaemia. See also AAR96146-81.
XX
SQ   Sequence   21 AA;

  Query Match             87.7%;  Score 57;  DB 17;  Length 21;
  Best Local Similarity   91.7%;  Pred. No. 0.0054;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 14
AAP90276
ID   AAP90276 standard; protein; 22 AA.
XX
AC   AAP90276;
XX
DT   17-MAY-1990  (first entry)
XX
DE   Antigen probe for human fibrinogen C-terminal alpha chain cleavage prods.
XX
KW   C-terminal; antigenic peptide; fibrinogen; human leukocyte elastase;
CC   connective tissue disease; alpha chain; probe;
XX
OS   Homo sapiens.
XX
PN   EP345906-A.
XX
PD   13-DEC-1989.
XX
PF   07-JUN-1989;   89EP-0201460.
XX
PR   10-JUN-1988;   88US-0205416.
PR   10-JUN-1988;   88US-0205417.
PR   10-JUN-1988;   88US-0205418.
XX
PA   (MERI ) MERCK AND CO. INC.
XX
PI   Dahlgren ME,  Mumford RA,  Boger JS,  Davies DTP;
XX
DR   WPI; 1989-365672/50.
XX
PT   New elastase-induced fibrinogen cleavage peptide(s) - for prodn. of
CC   new diagnostic antibodies.
XX
PS   Example 5; page 17; 33pp; English.
XX
CC   The synthetic peptide  corresponds to AAs 1-22 of human fibrinogen alpha
CC   chain. Probes with a tyrosine at the N-terminal (distal to the epitope)
CC   for coupling to 125. Probes may also be used to determine to evaluate the
CC   presence and amt. of human leukocyte elastase (hLE) cleavage prods. of
CC   human fibrinogen. Truncated versions of this sequence, eg AAs 5-21,
CC   9-21, 12-21, 14-21, 15-21, or 17-21; or 1-21,22,20,19,18, or 16 are used
CC   to determine antibody specificity and demonstrate that the specificity
CC   resides in AAs 17-21. hLE-induced cleavage of hF occurs in  eg
CC   connective tissue destructive diseases such as emphysema, chronic
CC   bronchitis, cystic fibrosis, arthritis, psoriasis, or atherosclerosis.
XX
SQ   Sequence   22 AA;

  Query Match             87.7%;  Score 57;  DB 10;  Length 22;
  Best Local Similarity   91.7%;  Pred. No. 0.0056;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 15
AAR96182
ID   AAR96182 standard; peptide; 22 AA.
XX
AC   AAR96182;
XX
```

DT 19-DEC-1996 (first entry)
XX
DE Fibrinogen epitope probe, represents alpha chain residues -1-21.
XX
KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
KW sputum; broncheoalveolar lavage fluid; assay; inhibitor; arthritis;
KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
KW chronic obstructive pulmonary disease; myelogenous leukaemia;
KW infantile respiratory distress syndrome; gout;
KW adult respiratory distress syndrome.
XX
OS Homo sapiens.
XX
PN WO9614580-A1.
XX
PD 17-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US13794.
XX
PR 06-JUN-1995; 95US-0469141.
PR 07-NOV-1994; 94US-0335524.
XX
PA (MERI) MERCK & CO INC.
XX
PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;
XX
DR WPI; 1996-251888/25.
XX
PT New isolated fibrinogen derived cleavage products - used for
PT detection of leukocyte elastase activity in disease diagnosis and
PT for evaluating elastase inhibitors
XX
PS Example 5; Page 41; 109pp; English.
XX
CC The sequences given in AAR96182-94 represent antigenic probes derived
CC from the first 21 amino acids of human fibrinogen. These probes are
CC used to determine antibody titre against other fibrinogen cleavage
CC products. The monospecific antibodies may be used to assay for the
CC formation of complimentary cleavage product antigens or epitopes in
CC whole blood or other body fluids, peritoneal fluid, sputum or
CC broncheoalveolar lavage fluid. The assay for cleavage products is
CC dependent upon the presence of HLE in the sample. This assay can also
CC be used for the evaluation of HLE inhibitors. The antibodies may be
CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
CC pulmonary disease, bronchiectasis, adult or infantile respiratory
CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.
XX
SQ Sequence 22 AA;

Query Match 87.7%; Score 57; DB 17; Length 22;
Best Local Similarity 91.7%; Pred. No. 0.0056;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      6 EGDFLAEGGGVR 17
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Search completed: February 10, 2003, 16:00:48
Job time : 83 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 15:59:27 ; Search time 15 Seconds
(without alignments)
25.500 Million cell updates/sec

Title: US-09-845-729-1
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	87.7	16	2	US-08-796-598-14	Sequence 14, Appl
2	57	87.7	16	2	US-08-447-175A-14	Sequence 14, Appl
3	57	87.7	16	3	US-08-469-141A-56	Sequence 56, Appl
4	57	87.7	16	5	PCT-US95-13794-56	Sequence 56, Appl
5	57	87.7	17	3	US-08-469-141A-46	Sequence 46, Appl
6	57	87.7	17	5	PCT-US95-13794-46	Sequence 46, Appl
7	57	87.7	18	3	US-08-469-141A-55	Sequence 55, Appl
8	57	87.7	18	5	PCT-US95-13794-55	Sequence 55, Appl
9	57	87.7	19	3	US-08-469-141A-54	Sequence 54, Appl
10	57	87.7	19	5	PCT-US95-13794-54	Sequence 54, Appl
11	57	87.7	20	1	US-08-288-657-1	Sequence 1, Appli
12	57	87.7	20	1	US-07-984-884-1	Sequence 1, Appli
13	57	87.7	20	1	US-08-481-810-1	Sequence 1, Appli
14	57	87.7	20	1	US-08-484-426-1	Sequence 1, Appli
15	57	87.7	20	2	US-08-480-818-1	Sequence 1, Appli
16	57	87.7	20	3	US-08-469-141A-53	Sequence 53, Appl
17	57	87.7	20	5	PCT-US95-13794-53	Sequence 53, Appl
18	57	87.7	21	3	US-08-469-141A-45	Sequence 45, Appl
19	57	87.7	21	5	PCT-US95-13794-45	Sequence 45, Appl
20	57	87.7	22	3	US-08-469-141A-44	Sequence 44, Appl
21	57	87.7	22	3	US-08-469-141A-52	Sequence 52, Appl
22	57	87.7	22	5	PCT-US95-13794-44	Sequence 44, Appl
23	57	87.7	22	5	PCT-US95-13794-52	Sequence 52, Appl
24	57	87.7	23	4	US-08-860-808E-25	Sequence 25, Appl
25	57	87.7	25	4	US-08-440-322-16	Sequence 16, Appl
26	57	87.7	25	4	US-08-440-331-16	Sequence 16, Appl
27	57	87.7	30	2	US-07-963-538B-9	Sequence 9, Appli
28	57	87.7	643	2	US-08-551-356-4	Sequence 4, Appli
29	57	87.7	643	5	PCT-US93-12687-4	Sequence 4, Appli
30	57	87.7	644	1	US-08-206-176-2	Sequence 2, Appli
31	57	87.7	847	4	US-09-373-157-4	Sequence 4, Appli
32	52	80.0	15	3	US-08-469-141A-6	Sequence 6, Appli
33	52	80.0	15	5	PCT-US95-13794-6	Sequence 6, Appli
34	52	80.0	28	6	5196404-16	Patent No. 5196404
35	47	72.3	10	6	5196404-18	Patent No. 5196404
36	47	72.3	10	6	5433940-25	Patent No. 5433940
37	46	70.8	17	2	US-08-792-553-11	Sequence 11, Appl
38	46	70.8	24	2	US-08-978-404B-48	Sequence 48, Appl
39	40	61.5	13	3	US-08-469-141A-47	Sequence 47, Appl
40	40	61.5	13	5	PCT-US95-13794-47	Sequence 47, Appl
41	36	55.4	11	3	US-08-592-500-39	Sequence 39, Appl
42	36	55.4	11	3	US-08-195-006-39	Sequence 39, Appl
43	36	55.4	11	5	PCT-US94-07644A-39	Sequence 39, Appl
44	36	55.4	14	4	US-08-860-808E-1	Sequence 1, Appli
45	36	55.4	420	1	US-08-391-259-7	Sequence 7, Appli

ALIGNMENTS

```
RESULT 1
US-08-796-598-14
; Sequence 14, Application US/08796598
; Patent No. 5827659
;  GENERAL INFORMATION:
;    APPLICANT:  PATTERSON, DALE H.
;    APPLICANT:  TARR, GEORGE E.
;    TITLE OF INVENTION:  METHODS AND APPARATUS FOR SEQUENCING
;    TITLE OF INVENTION:  POLYMERS USING MASS SPECTROMETRY.
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patent Administrator - Testa, Hurwitz &
;      ADDRESSEE:  Thibeault
;      STREET:  High Street Tower, 125 High Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/796,598
;      FILING DATE:  07-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/446,055
;      FILING DATE:  19-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FLYNN Esq., Kerry A.
;      REGISTRATION NUMBER:  33,693
;      REFERENCE/DOCKET NUMBER:  SYP-115
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-796-598-14

  Query Match            87.7%;  Score 57;  DB 2;  Length 16;
  Best Local Similarity  91.7%;  Pred. No. 0.00089;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 2
US-08-447-175A-14
; Sequence 14, Application US/08447175A
; Patent No. 5869240
;  GENERAL INFORMATION:
;    APPLICANT:  PATTERSON, DALE H.
;    TITLE OF INVENTION:  METHODS AND APPARATUS FOR SEQUENCING
;    TITLE OF INVENTION:  POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
;    TITLE OF INVENTION:  SPECTROMETRY.
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patent Administrator - Testa, Hurwitz &
;      ADDRESSEE:  Thibeault, LLP
;      STREET:  High Street Tower, 125 High Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,175A
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  422
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAUSCHENBACH, Kurt
;      REGISTRATION NUMBER:  40,137
;      REFERENCE/DOCKET NUMBER:  SYP-114
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-447-175A-14

  Query Match             87.7%;  Score 57;  DB 2;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.00089;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 3
US-08-469-141A-56
; Sequence 56, Application US/08469141A
; Patent No. 6124107
;  GENERAL INFORMATION:
;    APPLICANT:  MUMFORD, RICHARD A.
;    APPLICANT:  DAVIES, D.T. PHILIP
;    APPLICANT:  DAHLGREN, MARY E.
;    APPLICANT:  BOGER, JOSHUA S.
;    APPLICANT:  HUMES, JOHN L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DR. CHRISTINE E. CARTY
;      STREET:  126 E. LINCOLN AVENUE., P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,141A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARTY, CHRISTINE E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)-594-6734
;      TELEFAX:  (908)-594-4720
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-469-141A-56

  Query Match             87.7%;  Score 57;  DB 3;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.00089;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 4
PCT-US95-13794-56
; Sequence 56, Application PC/TUS9513794
;  GENERAL INFORMATION:
;    APPLICANT:  Mumford, Richard A.
;    APPLICANT:  Davies, D.T. Philip
;    APPLICANT:  Dahlgren, Mary E.
;    APPLICANT:  Boger, Joshua S.
;    APPLICANT:  Humes, John L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dr. Christine E. Carty
;      STREET:  126 E. Lincoln Avenue; P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13794
;      FILING DATE:  03-NOV-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carty, Christine E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IAY
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-6734
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
PCT-US95-13794-56

  Query Match             87.7%;  Score 57;  DB 5;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.00089;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 5
US-08-469-141A-46
; Sequence 46, Application US/08469141A
; Patent No. 6124107
;  GENERAL INFORMATION:
;    APPLICANT:  MUMFORD, RICHARD A.
;    APPLICANT:  DAVIES, D.T. PHILIP
;    APPLICANT:  DAHLGREN, MARY E.
;    APPLICANT:  BOGER, JOSHUA S.
;    APPLICANT:  HUMES, JOHN L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DR. CHRISTINE E. CARTY
;      STREET:  126 E. LINCOLN AVENUE., P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,141A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARTY, CHRISTINE E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)-594-6734
;      TELEFAX:  (908)-594-4720
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-469-141A-46

  Query Match             87.7%;  Score 57;  DB 3;  Length 17;
  Best Local Similarity   91.7%;  Pred. No. 0.00095;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      1 EGDFLAEGGGVR 12


RESULT 6
PCT-US95-13794-46
; Sequence 46, Application PC/TUS9513794
;  GENERAL INFORMATION:
;    APPLICANT:  Mumford, Richard A.
;    APPLICANT:  Davies, D.T. Philip
;    APPLICANT:  Dahlgren, Mary E.
;    APPLICANT:  Boger, Joshua S.
;    APPLICANT:  Humes, John L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dr. Christine E. Carty
;      STREET:  126 E. Lincoln Avenue; P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13794
;      FILING DATE:  03-NOV-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carty, Christine E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IAY
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-6734
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
PCT-US95-13794-46

  Query Match             87.7%;  Score 57;  DB 5;  Length 17;
  Best Local Similarity   91.7%;  Pred. No. 0.00095;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      1 EGDFLAEGGGVR 12


RESULT 7
US-08-469-141A-55
; Sequence 55, Application US/08469141A
; Patent No. 6124107
;  GENERAL INFORMATION:
;    APPLICANT:  MUMFORD, RICHARD A.
;    APPLICANT:  DAVIES, D.T. PHILIP
;    APPLICANT:  DAHLGREN, MARY E.
;    APPLICANT:  BOGER, JOSHUA S.
```

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;    APPLICANT:  HUMES, JOHN L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DR. CHRISTINE E. CARTY
;      STREET:  126 E. LINCOLN AVENUE., P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,141A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARTY, CHRISTINE E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)-594-6734
;      TELEFAX:  (908)-594-4720
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-469-141A-55

  Query Match             87.7%;  Score 57;  DB 3;  Length 18;
  Best Local Similarity   91.7%;  Pred. No. 0.001;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 8
PCT-US95-13794-55
; Sequence 55, Application PC/TUS9513794
;  GENERAL INFORMATION:
;    APPLICANT:  Mumford, Richard A.
;    APPLICANT:  Davies, D.T. Philip
;    APPLICANT:  Dahlgren, Mary E.
;    APPLICANT:  Boger, Joshua S.
;    APPLICANT:  Humes, John L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dr. Christine E. Carty
;      STREET:  126 E. Lincoln Avenue; P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13794
;      FILING DATE:  03-NOV-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carty, Christine E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IAY
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-6734
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
PCT-US95-13794-55

  Query Match             87.7%;  Score 57;  DB 5;  Length 18;
  Best Local Similarity   91.7%;  Pred. No. 0.001;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 9
US-08-469-141A-54
; Sequence 54, Application US/08469141A
; Patent No. 6124107
;  GENERAL INFORMATION:
;    APPLICANT:  MUMFORD, RICHARD A.
;    APPLICANT:  DAVIES, D.T. PHILIP
;    APPLICANT:  DAHLGREN, MARY E.
;    APPLICANT:  BOGER, JOSHUA S.
;    APPLICANT:  HUMES, JOHN L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DR. CHRISTINE E. CARTY
;      STREET:  126 E. LINCOLN AVENUE., P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,141A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARTY, CHRISTINE E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)-594-6734
;      TELEFAX:  (908)-594-4720
;  INFORMATION FOR SEQ ID NO:  54:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-469-141A-54

  Query Match             87.7%;  Score 57;  DB 3;  Length 19;
  Best Local Similarity   91.7%;  Pred. No. 0.0011;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 10
PCT-US95-13794-54
; Sequence 54, Application PC/TUS9513794
;  GENERAL INFORMATION:
;    APPLICANT:  Mumford, Richard A.
;    APPLICANT:  Davies, D.T. Philip
;    APPLICANT:  Dahlgren, Mary E.
;    APPLICANT:  Boger, Joshua S.
;    APPLICANT:  Humes, John L.
;    TITLE OF INVENTION:  ASSAY FOR MARKER OF HUMAN
;    TITLE OF INVENTION:  POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dr. Christine E. Carty
;      STREET:  126 E. Lincoln Avenue; P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13794
;      FILING DATE:  03-NOV-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carty, Christine E.
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  17461IAY
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-6734
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  54:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
PCT-US95-13794-54

  Query Match             87.7%;  Score 57;  DB 5;  Length 19;
  Best Local Similarity   91.7%;  Pred. No. 0.0011;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 11
US-08-288-657-1
; Sequence 1, Application US/08288657
; Patent No. 5424291
;  GENERAL INFORMATION:
;    APPLICANT:  Atrash, Butrus
;    APPLICANT:  Jones, David M.
;    APPLICANT:  Szelke, Michael
;    TITLE OF INVENTION:  New Isosteric Peptides
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Richard J. Sterner, Ph.D.
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/288,657
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/751,700
;      FILING DATE:  08-AUG-1991
;      APPLICATION NUMBER:  SE 9102462-0
;      FILING DATE:  28-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner Ph.D., Richard J.
;      REGISTRATION NUMBER:  35,372
;      REFERENCE/DOCKET NUMBER:  1103326-871
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-819-8783
;      TELEFAX:  212-354-8113
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..20
;      OTHER INFORMATION:  /note= "Peptide sequence containing
;      OTHER INFORMATION:  thrombin cleavage site in the human fibrinogen
;      OTHER INFORMATION:  A-alpha chain."
;    FEATURE:
;      NAME/KEY:  Cleavage-site
;      LOCATION:  16..17
US-08-288-657-1

  Query Match             87.7%;  Score 57;  DB 1;  Length 20;
  Best Local Similarity   91.7%;  Pred. No. 0.0011;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 12
US-07-984-884-1
; Sequence 1, Application US/07984884
; Patent No. 5614499
;  GENERAL INFORMATION:
;    APPLICANT:  Teger-Nilsson, Ann-Catrine E
;    APPLICANT:  Bylund, Ruth E
```

```
;    TITLE OF INVENTION:  New peptide derivatives
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White and Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/984,884
;      FILING DATE:  02-DEC-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner, Richard J
;      REGISTRATION NUMBER:  35, 372
;      REFERENCE/DOCKET NUMBER:  1103326-016
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)819-8200
;      TELEFAX:  (212)354-8113
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
US-07-984-884-1

  Query Match             87.7%;  Score 57;  DB 1;  Length 20;
  Best Local Similarity   91.7%;  Pred. No. 0.0011;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


RESULT 13
US-08-481-810-1
; Sequence 1, Application US/08481810
; Patent No. 5736521
;  GENERAL INFORMATION:
;    APPLICANT:  Teger-Nilsson, Ann-Catrine E
;    APPLICANT:  Bylund, Ruth E
;    TITLE OF INVENTION:  New peptide derivatives
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White and Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,810
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/984884
;      FILING DATE:  02-DEC-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner, Richard J
;      REGISTRATION NUMBER:  35,372
;      REFERENCE/DOCKET NUMBER:  1103326-016
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)819-8200
;      TELEFAX:  (212)354-8113
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
US-08-481-810-1

  Query Match             87.7%;  Score 57;  DB 1;  Length 20;
  Best Local Similarity   91.7%;  Pred. No. 0.0011;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


RESULT 14
US-08-484-426-1
; Sequence 1, Application US/08484426
; Patent No. 5747460
;  GENERAL INFORMATION:
;    APPLICANT:  Teger-Nilsson, Ann-Catrine E
;    APPLICANT:  Bylund, Ruth E
;    TITLE OF INVENTION:  New peptide derivatives
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White and Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,426
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/984884
;      FILING DATE:  02-DEC-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner, Richard J
;      REGISTRATION NUMBER:  35,372
;      REFERENCE/DOCKET NUMBER:  1103326-016
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)819-8200
;      TELEFAX:  (212)354-8113
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
US-08-484-426-1

  Query Match             87.7%;  Score 57;  DB 1;  Length 20;
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  Best Local Similarity   91.7%;  Pred. No. 0.0011;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


RESULT 15
US-08-480-818-1
; Sequence 1, Application US/08480818
; Patent No. 5955433
;  GENERAL INFORMATION:
;    APPLICANT:  Teger-Nilsson, Ann-Catrine E
;    APPLICANT:  Bylund, Ruth E
;    TITLE OF INVENTION:  New peptide derivatives
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White and Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,818
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/984884
;      FILING DATE:  02-DEC-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner, Richard J
;      REGISTRATION NUMBER:  35,372
;      REFERENCE/DOCKET NUMBER:  1103326-016
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)819-8200
;      TELEFAX:  (212)354-8113
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
US-08-480-818-1

  Query Match             87.7%;  Score 57;  DB 2;  Length 20;
  Best Local Similarity   91.7%;  Pred. No. 0.0011;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


Search completed: February 10, 2003, 16:07:45
Job time : 16 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 16:02:52 ; Search time 29 Seconds
(without alignments)
11.453 Million cell updates/sec

Title: US-09-845-729-1
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	87.7	12	9	US-09-845-725-1	Sequence 1, Appli
2	57	87.7	15	9	US-09-845-719A-1	Sequence 1, Appli
3	57	87.7	16	9	US-09-846-780-1	Sequence 1, Appli
4	57	87.7	16	9	US-09-826-290-352	Sequence 352, App
5	57	87.7	25	9	US-09-757-774-16	Sequence 16, Appl
6	57	87.7	360	10	US-09-925-297-587	Sequence 587, App
7	57	87.7	847	9	US-10-112-527-4	Sequence 4, Appli
8	52	80.0	10	9	US-09-846-350-1	Sequence 1, Appli
9	52	80.0	11	9	US-09-846-342-1	Sequence 1, Appli
10	46	70.8	17	9	US-10-057-505-11	Sequence 11, Appl
11	42	64.6	98	10	US-09-740-668A-18	Sequence 18, Appl
12	39	60.0	1164	10	US-09-834-792-5	Sequence 5, Appli
13	39	60.0	1165	9	US-10-026-188-8	Sequence 8, Appli
14	39	60.0	2039	9	US-10-192-584-7	Sequence 7, Appli
15	38	58.5	154	10	US-09-925-300-1763	Sequence 1763, Ap
16	36	55.4	359	9	US-09-972-758-2	Sequence 2, Appli
17	36	55.4	359	10	US-09-745-763-34	Sequence 34, Appl
18	36	55.4	426	10	US-09-864-761-42921	Sequence 42921, A
19	35.5	54.6	418	9	US-09-738-626-5679	Sequence 5679, Ap
20	35	53.8	621	10	US-09-815-242-11303	Sequence 11303, A
21	35	53.8	845	9	US-09-738-626-4347	Sequence 4347, Ap
22	35	53.8	2042	9	US-10-192-584-6	Sequence 6, Appli
23	34	52.3	37	10	US-09-813-345-7	Sequence 7, Appli
24	34	52.3	192	9	US-09-738-626-5432	Sequence 5432, Ap
25	34	52.3	211	10	US-09-925-302-467	Sequence 467, App
26	34	52.3	272	9	US-09-774-639-167	Sequence 167, App
27	34	52.3	487	10	US-09-841-132-349	Sequence 349, App
28	34	52.3	583	10	US-09-841-132-353	Sequence 353, App
29	34	52.3	821	10	US-09-841-132-195	Sequence 195, App
30	34	52.3	1294	10	US-09-815-242-13724	Sequence 13724, A
31	34	52.3	1770	10	US-09-841-132-444	Sequence 444, App
32	34	52.3	1776	10	US-09-841-132-179	Sequence 179, App
33	33	50.8	36	8	US-08-424-550B-579	Sequence 579, App
34	33	50.8	263	10	US-09-815-242-11707	Sequence 11707, A
35	33	50.8	293	10	US-09-861-205-2	Sequence 2, Appli
36	33	50.8	293	12	US-10-054-313-2	Sequence 2, Appli
37	33	50.8	304	9	US-09-738-626-3928	Sequence 3928, Ap
38	33	50.8	314	9	US-09-738-626-6390	Sequence 6390, Ap
39	33	50.8	355	10	US-09-815-242-11457	Sequence 11457, A
40	33	50.8	355	10	US-09-815-242-11620	Sequence 11620, A
41	33	50.8	424	9	US-09-843-905A-13	Sequence 13, Appl
42	33	50.8	479	10	US-09-925-300-1515	Sequence 1515, Ap
43	33	50.8	640	9	US-09-983-204-16	Sequence 16, Appl
44	33	50.8	696	10	US-09-809-790-2	Sequence 2, Appli
45	33	50.8	696	10	US-09-809-617-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-845-725-1
; Sequence 1, Application US/09845725
; Patent No. US20020161185A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 1206 DALTONS
; FILE REFERENCE: 2132.028
; CURRENT APPLICATION NUMBER: US/09/845,725
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-725-1

Query Match 87.7%; Score 57; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 1 EGDFLAEGGGVR 12

RESULT 2
US-09-845-719A-1
; Sequence 1, Application US/09845719A
; Patent No. US20020161179A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 1465 DALTONS
; FILE REFERENCE: 2132.035
; CURRENT APPLICATION NUMBER: US/09/845,719A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

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;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-845-719A-1

  Query Match             87.7%;  Score 57;  DB 9;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 0.0015;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      4 EGDFLAEGGGVR 15


RESULT 3
US-09-846-780-1
; Sequence 1, Application US/09846780
; Patent No. US20020160423A1
; GENERAL INFORMATION:
;  APPLICANT: Jackowski, George
;  TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
;  TITLE OF INVENTION:  OF 1536 DALTONS
;  FILE REFERENCE: 2132.039
;  CURRENT APPLICATION NUMBER: US/09/846,780
;  CURRENT FILING DATE:  2001-04-30
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-846-780-1

  Query Match             87.7%;  Score 57;  DB 9;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.0016;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 4
US-09-826-290-352
; Sequence 352, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
;  APPLICANT: Durham, L.Kathryn
;  APPLICANT:  Friedman, David L.
;  APPLICANT:  Herath, Herath Mudiyanselage Athula Chandrasiri
;  APPLICANT:  Kimmel, Lida H.
;  APPLICANT:  Parekh, Rajesh Bhikhu
;  APPLICANT:  Potter, David M.
;  APPLICANT:  Rohlff, Christian
;  APPLICANT:  Silber, B. Michael
;  APPLICANT:  Stiger, Thomas R.
;  APPLICANT:  Sunderland, P. Trey
;  APPLICANT:  Townsend, Robert Reid
;  APPLICANT:  White, Frost
;  APPLICANT:  Williams, Stephen A.
;  TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
;  TITLE OF INVENTION:  Uses Therefor, Including Diagnosis and Treatment of
;  TITLE OF INVENTION:  Alzheimer's Disease
;  FILE REFERENCE: 2572-1-001 N2
;  CURRENT APPLICATION NUMBER: US/09/826,290
;  CURRENT FILING DATE:  2001-04-30
;  PRIOR APPLICATION NUMBER: US 60/194,504
;  PRIOR FILING DATE: 2000-04-03
;  PRIOR APPLICATION NUMBER: US 60/253,647
;  PRIOR FILING DATE: 2000-11-28
;  NUMBER OF SEQ ID NOS: 492
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 352
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: homo sapien
US-09-826-290-352

  Query Match             87.7%;  Score 57;  DB 9;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.0016;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      5 EGDFLAEGGGVR 16


RESULT 5
US-09-757-774-16
; Sequence 16, Application US/09757774
; Publication No. US20020187156A1
; GENERAL INFORMATION:
;  APPLICANT: Dintzis, Howard M.
;  APPLICANT:  Dintzis, Renee
;  APPLICANT:  Blodgett, James
;  APPLICANT:  Cheronis, John
;  TITLE OF INVENTION: THERAPEUTIC SUPPRESSION OF SPECIFIC IMMUNE RESPONSES BY
;  TITLE OF INVENTION:  ADMINISTRATION OF OLIGOMERIC FORMS OF ANTIGEN OF CONTROLLED
;  TITLE OF INVENTION:  CHEMISTRY
;  FILE REFERENCE: 07265/124004
;  CURRENT APPLICATION NUMBER: US/09/757,774
;  CURRENT FILING DATE:  2001-01-09
;  PRIOR APPLICATION NUMBER: US 08/440,322
;  PRIOR FILING DATE: 1995-05-12
;  PRIOR APPLICATION NUMBER: US 07/808,797
;  PRIOR FILING DATE: 1991-12-17
;  PRIOR APPLICATION NUMBER: US 07/628,858
;  PRIOR FILING DATE: 1990-12-17
;  PRIOR APPLICATION NUMBER: US 07/354,710
;  PRIOR FILING DATE: 1989-05-22
;  PRIOR APPLICATION NUMBER: US 07/248,293
;  PRIOR FILING DATE: 1988-09-21
;  PRIOR APPLICATION NUMBER: US 06/869,808
;  PRIOR FILING DATE: 1986-05-29
;  PRIOR APPLICATION NUMBER: US 06/460,266
;  PRIOR FILING DATE: 1983-01-24
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 25
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(25)
;   OTHER INFORMATION: Xaa = O-ACA/Pro
US-09-757-774-16

  Query Match             87.7%;  Score 57;  DB 9;  Length 25;
  Best Local Similarity   91.7%;  Pred. No. 0.0025;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ESDFLAEGGGVR 13
          | ||||||||||
Db      7 EGDFLAEGGGVR 18


RESULT 6
US-09-925-297-587
; Sequence 587, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA105
;  CURRENT APPLICATION NUMBER: US/09/925,297
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;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05989
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 928
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 587
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (15)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (315)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (325)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (326)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (327)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (339)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-587

  Query Match             87.7%;  Score 57;  DB 10;  Length 360;
  Best Local Similarity   91.7%;  Pred. No. 0.036;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db      45 EGDFLAEGGGVR 56


RESULT 7
US-10-112-527-4
; Sequence 4, Application US/10112527
; Patent No. US20020168722A1
; GENERAL INFORMATION:
;  APPLICANT: Grieninger, Gerd
;  APPLICANT:  Applegate, Dianne
;  APPLICANT:  Stoike-Steben, Lara
;  TITLE OF INVENTION: No. US20020168722A1el Cleaved Fragments of Fibrinogen
;  FILE REFERENCE: Docket 454-24 CON
;  CURRENT APPLICATION NUMBER: US/10/112,527
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 09/373,157
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 847
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-112-527-4

  Query Match             87.7%;  Score 57;  DB 9;  Length 847;
  Best Local Similarity   91.7%;  Pred. No. 0.086;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


RESULT 8
US-09-846-350-1
; Sequence 1, Application US/09846350
; Patent No. US20020161188A1
; GENERAL INFORMATION:
;  APPLICANT: Jackowski, George
;  TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having a Molecular
;  TITLE OF INVENTION:  of 1020 Daltons
;  FILE REFERENCE: 2132.025
;  CURRENT APPLICATION NUMBER: US/09/846,350
;  CURRENT FILING DATE:  2001-04-30
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-846-350-1

  Query Match             80.0%;  Score 52;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0063;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 DFLAEGGGVR 13
           ||||||||||
Db       1 DFLAEGGGVR 10


RESULT 9
US-09-846-342-1
; Sequence 1, Application US/09846342
; Patent No. US20020160422A1
; GENERAL INFORMATION:
;  APPLICANT: Jackowski, George
;  TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
;  TITLE OF INVENTION:  OF 1077 DALTONS
;  FILE REFERENCE: 2132.026
;  CURRENT APPLICATION NUMBER: US/09/846,342
;  CURRENT FILING DATE:  2001-04-30
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-846-342-1

  Query Match             80.0%;  Score 52;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0069;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 DFLAEGGGVR 13
           ||||||||||
Db       2 DFLAEGGGVR 11


RESULT 10
US-10-057-505-11
; Sequence 11, Application US/10057505
; Patent No. US20020164674A1
; GENERAL INFORMATION:
;  APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
;  APPLICANT:  AURORA BIOSCIENCES CORPORATION
;  APPLICANT:  TSIEN, Roger
;  APPLICANT:  HEIM, Roger
;  APPLICANT:  CUBITT, Andrew
;  TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
;  FILE REFERENCE: REGEN1260-3
;  CURRENT APPLICATION NUMBER: US/10/057,505
;  CURRENT FILING DATE:  2002-01-25
;  PRIOR APPLICATION NUMBER: US 08/792,553
;  PRIOR FILING DATE: 1997-01-31
;  PRIOR APPLICATION NUMBER: US 09/396,003
;  PRIOR FILING DATE: 1999-09-13
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;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Linker moiety
US-10-057-505-11

  Query Match             70.8%;  Score 46;  DB 9;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 FLAEGGGVR 13
           |||||||||
Db       1 FLAEGGGVR 9


RESULT 11
US-09-740-668A-18
; Sequence 18, Application US/09740668A
; Patent No. US20020076700A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard
;  TITLE OF INVENTION: No. US20020076700A1el polypeptides and nucleic acids encoding sam
;  FILE REFERENCE: 15966-537 CIP
;  CURRENT APPLICATION NUMBER: US/09/740,668A
;  CURRENT FILING DATE:  2000-12-18
;  PRIOR APPLICATION NUMBER: PCT/US99/29584
;  PRIOR FILING DATE: 1999-12-17
;  PRIOR APPLICATION NUMBER: 09/465,512
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: 60/113,485
;  PRIOR FILING DATE: 1999-12-21
;  PRIOR APPLICATION NUMBER: 60/112,837
;  PRIOR FILING DATE: 1998-12-18
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-740-668A-18

  Query Match             64.6%;  Score 42;  DB 10;  Length 98;
  Best Local Similarity   63.6%;  Pred. No. 2.7;
  Matches    7;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 SDFLAEGGGVR 13
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Db      50 ADFLGQGGGVQ 60


RESULT 12
US-09-834-792-5
; Sequence 5, Application US/09834792
; Patent No. US20020037515A1
; GENERAL INFORMATION:
;  APPLICANT: Mount Sinai School of Medicine of NYU
;  TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
;  TITLE OF INVENTION:  CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
;  FILE REFERENCE: AP32911 070165.0589
;  CURRENT APPLICATION NUMBER: US/09/834,792
;  CURRENT FILING DATE:  2001-04-13
;  PRIOR APPLICATION NUMBER: 60/197,491
;  PRIOR FILING DATE: 2000-04-17
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1164
;   TYPE: PRT
;   ORGANISM: Human
US-09-834-792-5

  Query Match             60.0%;  Score 39;  DB 10;  Length 1164;
  Best Local Similarity   61.5%;  Pred. No. 1e+02;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
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Db    1117 SVADVLAQGGGPR 1129


RESULT 13
US-10-026-188-8
; Sequence 8, Application US/10026188
; Patent No. US20020164645A1
; GENERAL INFORMATION:
;  APPLICANT: Zuker, Charles S.
;  APPLICANT:  Zhang, Yifeng
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
;  TITLE OF INVENTION:  Ion Channel
;  FILE REFERENCE: 02307E-114910US
;  CURRENT APPLICATION NUMBER: US/10/026,188
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: US 60/259,379
;  PRIOR FILING DATE: 2000-12-29
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 1165
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human ltrpc6
US-10-026-188-8

  Query Match             60.0%;  Score 39;  DB 9;  Length 1165;
  Best Local Similarity   61.5%;  Pred. No. 1e+02;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
           | :| ||:||| |
Db    1118 SVADVLAQGGGPR 1130


RESULT 14
US-10-192-584-7
; Sequence 7, Application US/10192584
; Publication No. US20030027987A1
;   GENERAL INFORMATION:
;        APPLICANT: TOKUNAGA, Eiji
;                   SAKAGUCHI, Masashi
;                   MATSUO, Kazuo
;                   HAMADA, Fukusaburo
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
;                            PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 624 Ninth Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20001
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: Patent In Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/192,584
;             FILING DATE: 11-Jul-2002
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;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/077,098
;             FILING DATE: 19-May-1998
;             APPLICATION NUMBER: PCT/JP97/03222
;             FILING DATE: 12-SEP-1997
;             APPLICATION NUMBER: JP 27,148/1996
;             FILING DATE: 19-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: KORNBAU, Anne M.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: TOKUNAGA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2039 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-192-584-7

  Query Match             60.0%;  Score 39;  DB 9;  Length 2039;
  Best Local Similarity   61.5%;  Pred. No. 1.8e+02;
  Matches    8;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
           || | |  ||||:
Db     786 SEIDLLQNGGGVQ 798


RESULT 15
US-09-925-300-1763
; Sequence 1763, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
;  APPLICANT: Craig Rosen,
;  APPLICANT:  Steve Ruben
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA101
;  CURRENT APPLICATION NUMBER: US/09/925,300
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05988
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1890
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1763
;   LENGTH: 154
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (147)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1763

  Query Match             58.5%;  Score 38;  DB 10;  Length 154;
  Best Local Similarity   72.7%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGG 11
             | :||||| ||
Db      28 SLTDFLAEDGG 38


Search completed: February 10, 2003, 16:15:30
Job time : 29 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 15:58:46 ; Search time 16 Seconds
(without alignments)
78.109 Million cell updates/sec

Title: US-09-845-729-1
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	93.8	16	2	H29501	fibrinopeptide A -
2	57	87.7	16	2	C28854	fibrinopeptide A -
3	57	87.7	16	2	A24180	fibrinogen alpha c
4	57	87.7	16	2	B24180	fibrinogen alpha c
5	57	87.7	16	2	A28854	fibrinopeptide A -
6	57	87.7	16	2	B28854	fibrinopeptide A -
7	57	87.7	16	2	A29501	fibrinopeptide A -
8	57	87.7	644	1	FGHUA	fibrinogen alpha c
9	57	87.7	866	2	D44234	fibrinogen alpha c
10	52	80.0	15	2	F29501	fibrinopeptide A -
11	51	78.5	16	2	G29501	fibrinopeptide A -
12	51	78.5	28	2	A05296	fibrinogen alpha c
13	49	75.4	17	2	E29501	fibrinopeptide A -
14	48	73.8	15	2	I29501	fibrinopeptide A -
15	48	73.8	19	2	B29501	fibrinopeptide A -
16	48	73.8	19	2	C29501	fibrinopeptide A -
17	48	73.8	311	2	A05294	fibrinogen alpha c
18	40	61.5	15	2	JP0101	fibrinogen alpha c
19	40	61.5	280	2	H89800	hypothetical prote
20	39	60.0	236	2	S48867	dimethylallyltrans
21	39	60.0	245	2	AG0701	Orf 245 protein [i
22	39	60.0	271	2	S18730	aminoglycoside N3'
23	39	60.0	324	2	D70943	hypothetical prote
24	39	60.0	705	2	T31157	hypothetical prote
25	38.5	59.2	732	2	AB2732	conserved hypothet
26	38.5	59.2	741	2	B97513	probable secreted
27	38	58.5	575	2	T48224	probable homeodoma
28	38	58.5	611	1	S12566	translation initia
29	38	58.5	652	2	AD2316	hypothetical prote
30	38	58.5	669	2	A72718	hypothetical prote
31	38	58.5	686	2	T08919	hypothetical prote
32	38	58.5	727	2	T08920	hypothetical prote
33	38	58.5	742	2	T00371	hypothetical prote
34	37	56.9	149	2	G85534	hypothetical prote
35	37	56.9	149	2	C90684	hypothetical prote
36	37	56.9	164	2	E70639	hypothetical prote
37	37	56.9	302	2	F90526	hypothetical prote
38	37	56.9	363	2	G71544	hypothetical prote
39	37	56.9	410	2	F96683	hypothetical prote
40	37	56.9	412	2	S28423	isocitrate dehydro
41	37	56.9	415	2	S65065	isocitrate dehydro
42	37	56.9	416	2	S47013	isocitrate dehydro
43	37	56.9	416	2	A96585	NADP specific isoc
44	37	56.9	421	2	D69643	imidazolone-5-prop
45	37	56.9	433	2	T09619	isocitrate dehydro

ALIGNMENTS

RESULT 1
H29501
fibrinopeptide A - gray seal
C;Species: Halichoerus grypus (gray seal)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C;Accession: H29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: H29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BLO>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi

Query Match 93.8%; Score 61; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2 ESDFLAEGGGVR 13
           ||||||||||||
Db       5 ESDFLAEGGGVR 16
```

RESULT 2
C28854
fibrinopeptide A - gelada baboon
C;Species: Theropithecus gelada (gelada baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C;Accession: C28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropith
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: C28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16
```

RESULT 3
A24180
fibrinogen alpha chain - Japanese macaque (fragment)
N;Contains: fibrinopeptide A

C;Species: Macaca fuscata (Japanese macaque)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 26-Jan-1996
C;Accession: A24180
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E
uenons, and baboons.
A;Reference number: A91990; MUID:85289140; PMID:3928610
A;Accession: A24180
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 4
B24180
fibrinogen alpha chain - red guenon (fragment)
N;Contains: fibrinopeptide A
C;Species: Erythrocebus patas (red guenon, hussar)
C;Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C;Accession: B24180
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E
uenons, and baboons.
A;Reference number: A91990; MUID:85289140; PMID:3928610
A;Accession: B24180
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 5
A28854
fibrinopeptide A - olive baboon
C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C;Accession: A28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: A28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 6
B28854
fibrinopeptide A - hamadryas baboon
C;Species: Papio hamadryas (hamadryas baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C;Accession: B28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: B28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 7
A29501
fibrinopeptide A - baboon
C;Species: Papio sp. (baboon)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 26-Jan-1996
C;Accession: A29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: A29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BLO>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 8
FGHUA
fibrinogen alpha chain precursor, short splice form [validated] - human
N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide A
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 30-Jun-1987 #text_change 08-Dec-2000
C;Accession: A93956; A43568; A90468; I84456; A44234; C44234; B94433; A90433; B94309; S19
R;Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A;Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains: ev
A;Reference number: A93956; MUID:83247396; PMID:6575389
A;Accession: A93956
A;Molecule type: mRNA
A;Residues: 1-644 <KAN>
A;Cross-references: GB:J00128; NID:g182425; PIDN:AAA52427.1; PID:g182426
A;Note: the authors translated the codon GAG for residue 247 as Gly, GGA for residue 438
R;Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A;Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A;Reference number: A43568; MUID:91344740; PMID:2102623
A;Accession: A43568
A;Molecule type: DNA
A;Residues: 1-330,'A',332-644 <CHU>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
R;Rixon, M.W.; Chan, W.Y.; Davie, E.W.; Chung, D.W.

Biochemistry 22, 3237-3244, 1983
A;Title: Characterization of a complementary deoxyribonucleic acid coding for the alpha
A;Reference number: A90468; MUID:83283432; PMID:6688355
A;Accession: A90468
A;Molecule type: mRNA
A;Residues: 1-330,'A',332-629 <RIX>
A;Cross-references: GB:J00127; NID:g182423; PIDN:AAA52426.1; PID:g182424
R;Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A;Title: Isolation and characterisation of cDNA clones for the Aalpha- and gamma-chains
A;Reference number: I37393; MUID:84069777; PMID:6689067
A;Accession: I84456
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 110-156 <RES>
A;Cross-references: GB:K02272; NID:g182427; PIDN:AAA52428.1; PID:g182428
R;Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
Biochemistry 31, 11968-11972, 1992
A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove
A;Reference number: A44234; MUID:93090725; PMID:1457396
A;Accession: A44234
A;Molecule type: mRNA
A;Residues: 1-51 <FU1>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
A;Note: sequence extracted from NCBI backbone (NCBIN:119912, NCBIN:119914, NCBIP:119918)
A;Accession: C44234
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 605-644 <FU2>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
A;Note: sequence extracted from NCBI backbone (NCBIP:119920)
R;Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
in Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe
A;Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
A;Reference number: A94433
A;Accession: B94433
A;Molecule type: protein
A;Residues: 20-214,'RS',217-298,'G',300-303,'G',305-629 <HEN>
R;Watt, K.W.K.; Cottrell, B.A.; Strong, D.D.; Doolittle, R.F.
Biochemistry 18, 5410-5416, 1979
A;Title: Amino acid sequences studies on the alpha chain of human fibrinogen. Overlappin
A;Reference number: A90433; MUID:80088231; PMID:518846
A;Contents: disulfide bonds
A;Accession: A90433
A;Molecule type: protein
A;Residues: 20-146,'Q',148-195,'N',197-230,'N',232-316,'SG',319-406,'D',408,'N',410-629
R;Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A;Reference number: A94309; MUID:76225080; PMID:936108
A;Contents: variant, and disulfide bonds
A;Accession: B94309
A;Molecule type: protein
A;Residues: 20-65,'T',67-629 <BLO>
R;Dewey, R.S.; Liesch, J.M.; Williams, H.R.; Sugg, E.E.; Dolan, C.A.; Davies, P.; Mumfor
Biochem. J. 281, 519-524, 1992
A;Title: Purification and characterization by fast-atom-bombardment mass spectrometry of
incubation with calcium ionophore A23187.
A;Reference number: S19297; MUID:92143822; PMID:1736899
A;Accession: S19297
A;Molecule type: protein
A;Residues: 20-40 <DEW>
R;Retzios, A.D.; Markland Jr., F.S.
Thromb. Res. 52, 541-552, 1988
A;Title: A direct-acting fibrinolytic enzyme from the venom of Agkistrodon contortrix co
A;Reference number: A60905; MUID:89162316; PMID:3232124
A;Accession: A60905
A;Molecule type: protein
A;Residues: 433-451 <RET>
R;Fretto, L.J.; Ferguson, E.W.; Steinman, H.M.; McKee, P.A.
J. Biol. Chem. 253, 2184-2195, 1978
A;Title: Localization of the alpha-chain cross-link acceptor sites of human fibrin.
A;Reference number: A92225; MUID:78130085; PMID:632262
A;Contents: annotation; cross-linking acceptor sites
R;Cottrell, B.A.; Strong, D.D.; Watt, K.W.K.; Doolittle, R.F.
Biochemistry 18, 5405-5410, 1979
A;Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Exact locat
A;Reference number: A90432; MUID:80088230; PMID:518845
A;Contents: annotation; cross-linking acceptor sites
R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A;Title: Covalent structure of fibrinogen.
A;Reference number: A90037; MUID:83254370; PMID:6575689
A;Contents: annotation; review, disulfide bonds
R;Itarte, E.; Plana, M.; Guasch, M.D.; Martos, C.
Biochem. Biophys. Res. Commun. 117, 631-636, 1983
A;Title: Phosphorylation of fibrinogen by casein kinase 1.
A;Reference number: A90116; MUID:84104274; PMID:6318767
A;Contents: annotation; phosphorylation
A;Note: about one-third of alpha chain molecules in blood were found to be phosphorylate
R;Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A;Title: Fibrinogen and fibrin.
A;Reference number: A90041; MUID:84305751; PMID:6383194
A;Contents: annotation; review, EM structure, polymerization, ligands
R;Kimura, S.; Aoki, N.
J. Biol. Chem. 261, 15591-15595, 1986
A;Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
A;Reference number: A92565; MUID:87057190; PMID:2877981
A;Contents: annotation; cross-linking site for alpha-2-plasmin inhibitor
R;Krishnamurthi, S.; Dickens, T.A.; Patel, Y.; Wheeler-Jones, C.P.D.; Kakkar, V.V.
Biochem. Biophys. Res. Commun. 163, 1256-1264, 1989
A;Title: The fibrinogen-derived peptide (RGDS) prevents proteolytic degradation of prote
A;Reference number: A33261; MUID:89392031; PMID:2783136
A;Contents: annotation; activity of cell attachment (R-G-D) motif
R;Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-te
A;Reference number: A37117; MUID:90337977; PMID:2143188
A;Contents: annotation; hementin cleavage site
A;Note: hementin, a protease from Haementeria ghilianii, the giant South American leech,
R;Staendker, L.; Sillard, R.; Bensch, K.W.; Ruf, A.; Raida, M.; Schulz-Knappe, P.; Schep
Biochem. Biophys. Res. Commun. 215, 896-902, 1995
A;Title: In vivo degradation of human fibrinogen A alpha: Detection of cleavage sites an
A;Reference number: JC4334; MUID:96027996; PMID:7488058
A;Contents: annotation; composition and amino-terminal sequences of carboxyl end peptide
C;Comment: Unlike the beta and gamma chains, the alpha chain is not glycosylated.
C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: See PIR:D44234 for the minor alternative splice form.
C;Genetics:
A;Gene: GDB:FGA
A;Cross-references: GDB:119129; OMIM:134820
A;Map position: 4q28-4q28
A;Introns: 18/3; 60/3; 122/1; 171/2
A;Note: the list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha, beta (see
ins are contained in the core. Two three-chain coiled coils emerge from this core and co
from the distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C;Keywords: alternative splicing; blood coagulation; coiled coil; glycoprotein; liver; pl
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-629/Product: fibrinogen alpha chain #status experimental <MAT>
F;20-35/Product: fibrinopeptide A #status experimental <APT>
F;36-629/Product: fibrin alpha chain #status experimental <FGA>
F;36-38/Region: polymerization site, binding to the distal domain of the gamma chain of
F;57-185/Domain: fibrinogen disulfide ring homology <FDR>
F;591-593/Region: cell attachment (R-G-D) motif
F;22,460/Binding site: phosphate (Ser) (covalent) #status experimental

F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F;47/Disulfide bonds: interchain (to alpha-47) #status experimental
F;55/Disulfide bonds: interchain (to beta-95) #status experimental
F;64/Disulfide bonds: interchain (to gamma-49) #status experimental
F;68/Disulfide bonds: interchain (to beta-106) #status experimental
F;180/Disulfide bonds: interchain (to gamma-165) #status experimental
F;184/Disulfide bonds: interchain (to beta-223) #status experimental
F;288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F;322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
F;347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
F;461-491/Disulfide bonds: #status experimental
F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status

Query Match 87.7%; Score 57; DB 1; Length 644;
Best Local Similarity 91.7%; Pred. No. 0.039;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db      24 EGDFLAEGGGVR 35
```

RESULT 9
D44234
fibrinogen alpha chain precursor, extended splice form - human
N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide A
C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 19-Jan-2001
C;Accession: D44234; B44234
R;Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
Biochemistry 31, 11968-11972, 1992
A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove
A;Reference number: A44234; MUID:93090725; PMID:1457396
A;Accession: D44234
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA; DNA
A;Residues: 1-866 <FU1>
A;Cross-references: GB:M58569; NID:g182406; PID:g182407
A;Note: neither the complete nucleic acid sequence nor the complete translation are show
A;Accession: B44234
A;Molecule type: mRNA; DNA
A;Residues: 605-866 <FU2>
A;Note: sequence extracted from NCBI backbone (NCBIP:119917)
C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: See PIR:FGHUA for the major splice form. It is not known whether this form is
C;Genetics:
A;Gene: GDB:FGA
A;Cross-references: GDB:119129; OMIM:134820
A;Map position: 4q28-4q28
A;Introns: 18/3; 60/3; 122/1; 171/2
A;Note: the list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentica
ntained in the core. Two three-chain coiled coils emerge from this core and connect it t
distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
C;Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
F;20-35/Product: fibrinopeptide A #status experimental <APT>
F;36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
F;57-185/Domain: fibrinogen disulfide ring homology <FDR>
F;591-593/Region: cell attachment (R-G-D) motif
F;629-863/Domain: fibrinogen beta/gamma homology <FBG>
F;22,460/Binding site: phosphate (Ser) (covalent) #status experimental

F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F;47/Disulfide bonds: interchain (to alpha-47) #status experimental
F;55/Disulfide bonds: interchain (to beta-95) #status experimental
F;64/Disulfide bonds: interchain (to gamma-49) #status experimental
F;68/Disulfide bonds: interchain (to beta-106) #status experimental
F;180/Disulfide bonds: interchain (to gamma-165) #status experimental
F;184/Disulfide bonds: interchain (to beta-223) #status experimental
F;288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F;322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
F;347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
F;461-491/Disulfide bonds: #status experimental
F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status
F;686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.7%; Score 57; DB 2; Length 866;
Best Local Similarity 91.7%; Pred. No. 0.053;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db      24 EGDFLAEGGGVR 35
```

RESULT 10
F29501
fibrinopeptide A - wombat
C;Species: Vombatidae gen. sp. (wombat)
C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C;Accession: F29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: F29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <BLO>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 80.0%; Score 52; DB 2; Length 15;
Best Local Similarity 76.9%; Pred. No. 0.0056;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1 SESDFLAEGGGVR 13
           :|  |||||||||
Db       3 TEGSFLAEGGGVR 15
```

RESULT 11
G29501
fibrinopeptide A - bear
C;Species: Ursus sp. (bear)
C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C;Accession: G29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: G29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BLO>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi

Query Match 78.5%; Score 51; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 0.009;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 ESDFLAEGGGVR 13
           | :|:|||||||
Db       5 EGEFIAEGGGVR 16
```

RESULT 12
A05296

fibrinogen alpha chain - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 25-Oct-1996
C;Accession: A94308; A03118; A37511; A05296; B37511; C03118
R;Birken, S.; Wilner, G.D.; Canfield, R.E.
Thromb. Res. 7, 599-610, 1975
A;Title: Studies of the structure of canine fibrinogen.
A;Reference number: A94308; MUID:76081726; PMID:1198547
A;Accession: A94308
A;Molecule type: protein
A;Residues: 1-28 <BIR>
R;Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A;Title: Studies on fibrinopeptides from mammals.
A;Reference number: A03118
A;Accession: A03118
A;Molecule type: protein
A;Residues: 1-16 <BLO>
R;Osbahr Jr., A.J.; Colman, R.W.; Laki, K.; Gladner, J.A.
Biochem. Biophys. Res. Commun. 14, 555-558, 1964
A;Reference number: A37511; MUID:66020594; PMID:5836555
A;Accession: A37511
A;Molecule type: protein
A;Residues: 1,'D',3,'EGKQ',8-16 <OSB>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C;Keywords: blood coagulation; liver; phosphoprotein; plasma
F;1-16/Product: fibrinopeptide A #status experimental <APT>
F;3/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

  Query Match 78.5%; Score 51; DB 2; Length 28;
  Best Local Similarity 75.0%; Pred. No. 0.016;
  Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| :|:|||||||
Db 5 EGEFIAEGGGVR 16

RESULT 13
E29501
fibrinopeptide A - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C;Accession: E29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: E29501
A;Molecule type: protein
A;Residues: 1-17 <BLO>
R;Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A;Title: Studies on fibrinopeptides from mammals.
A;Reference number: A03118
A;Contents: annotation; confirmation of species assignment
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi

  Query Match 75.4%; Score 49; DB 2; Length 17;
  Best Local Similarity 75.0%; Pred. No. 0.022;
  Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
: :||||||||||
Db 6 KGEFLAEGGGVR 17

RESULT 14
I29501
fibrinopeptide A - kangaroo
C;Species: Macropus sp. (kangaroo)
C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C;Accession: I29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: I29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <BLO>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

  Query Match 73.8%; Score 48; DB 2; Length 15;
  Best Local Similarity 75.0%; Pred. No. 0.029;
  Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| |:|||||||
Db 4 EGTFIAEGGGVR 15

RESULT 15
B29501
fibrinopeptide A - European moose
C;Species: Alces alces alces (European moose, elk)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C;Accession: B29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: B29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <BLO>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi

  Query Match 73.8%; Score 48; DB 2; Length 19;
  Best Local Similarity 90.0%; Pred. No. 0.037;
  Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DFLAEGGGVR 13
:|||||||||
Db 10 EFLAEGGGVR 19

Search completed: February 10, 2003, 16:07:25
Job time : 18 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 15:57:26 ; Search time 11 Seconds
(without alignments)
49.017 Million cell updates/sec

Title: US-09-845-729-1
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	87.7	16	1	FIBA_MACFU	P12803 macaca fusc
2	57	87.7	19	1	FIBA_CEREL	P14446 cervus elap
3	57	87.7	866	1	FIBA_HUMAN	P02671 homo sapien
4	56	86.2	16	1	FIBA_CERSI	P14535 ceratotheri
5	54	83.1	16	1	FIBA_TAPTE	P14536 tapirus ter
6	53	81.5	16	1	FIBA_HYLLA	P14453 hylobates l
7	53	81.5	18	1	FIBA_CAMDR	P14444 camelus dro
8	53	81.5	19	1	FIBA_BISBO	P14441 bison bonas
9	53	81.5	19	1	FIBA_CERNI	P14447 cervus nipp
10	51	78.5	16	1	FIBA_FELCA	P14450 felis silve
11	51	78.5	28	1	FIBA_CANFA	P02673 canis famil
12	49	75.4	17	1	FIBA_PIG	P14460 sus scrofa
13	49	75.4	18	1	FIBA_LAMGL	P14454 lama glama
14	48	73.8	15	1	FIBA_SYNCA	P14463 syncerus ca
15	48	73.8	16	1	FIBA_EQUAS	P14449 equus asinu
16	48	73.8	16	1	FIBA_MANLE	P14455 mandrillus
17	48	73.8	16	1	FIBA_ODOHE	P14459 odocoileus
18	48	73.8	19	1	FIBA_BUBBU	P14442 bubalus bub
19	48	73.8	19	1	FIBA_SHEEP	P14451 ovis aries
20	48	73.8	596	1	FIBA_BOVIN	P02672 bos taurus
21	47	72.3	14	1	FIBA_HORSE	P14452 equus cabal
22	45	69.2	19	1	FIBA_MUNMU	P14457 muntiacus m
23	40	61.5	15	1	FIBA_ANAPL	P12801 anas platyr
24	40	61.5	1696	1	PCK5_BRACL	Q9nj15 branchiosto
25	39	60.0	13	1	FIBA_CAVPO	P14445 cavia porce
26	39	60.0	236	1	IPT_ERWHE	Q47851 erwinia her
27	39	60.0	271	1	AAC3_PSEAE	P29808 pseudomonas
28	38	58.5	611	1	IF4B_HUMAN	P23588 homo sapien
29	38	58.5	742	1	SUN2_HUMAN	Q9uh99 homo sapien
30	37	56.9	19	1	FIBA_RANTA	P14462 rangifer ta
31	37	56.9	413	1	IDHC_SOYBN	Q06197 glycine max
32	37	56.9	415	1	IDHC_TOBAC	P50218 nicotiana t
33	37	56.9	416	1	IDHC_SOLTU	P50217 solanum tub
34	37	56.9	421	1	HUTI_BACSU	P42084 bacillus su
35	37	56.9	421	1	HUTI_STRPY	P58080 streptococc
36	37	56.9	433	1	IDHP_MEDSA	Q40345 medicago sa
37	36	55.4	16	1	FIBA_MUSVI	P14458 mustela vis
38	36	55.4	278	1	YKJ5_YEAST	P28320 saccharomyc
39	36	55.4	399	1	HUTI_DEIRA	Q9rz05 deinococcus
40	36	55.4	417	1	HUTI_HALN1	Q9hqd6 halobacteri
41	36	55.4	477	1	GLGA_RHOSH	Q9rnh6 rhodobacter
42	36	55.4	507	1	VL2_HPV1A	P03105 human papil
43	36	55.4	757	1	PPB2_MOUSE	O35385 mus musculu
44	35	53.8	218	1	Y010_MYCGE	P47256 mycoplasma
45	35	53.8	294	1	YQGI_BACSU	P46340 bacillus su

ALIGNMENTS

RESULT 1
FIBA_MACFU
ID FIBA_MACFU STANDARD; PRT; 16 AA.
AC P12803;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Macaca fuscata fuscata (Japanese macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey),
OS Macaca mulatta (Rhesus macaque),
OS Cercopithecus aethiops (Green monkey) (Grivet),
OS Erythrocebus patas (Red guenon) (Hussar),
OS Papio anubis (Olive baboon),
OS Papio hamadryas (Hamadryas baboon), and
OS Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9543, 9541, 9544, 9534, 9538, 9555, 9557, 9565;
RN [1]
RP SEQUENCE.
RC SPECIES=E.patas, and M.fuscata;
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
RN [2]
RP SEQUENCE.
RC SPECIES=P.anubis, P.hamadryas, and T.gelada;
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
RN [3]
RP SEQUENCE.
RC SPECIES=C.aethiops, M.mulatta, and M.fascicularis;
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; A24180; A24180.

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DR   PIR; B24180; B24180.
DR   PIR; A28854; A28854.
DR   PIR; B28854; B28854.
DR   PIR; C28854; C28854.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1551 MW;  49E8CBB63EA04DD3 CRC64;

  Query Match             87.7%;  Score 57;  DB 1;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.00034;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db       5 EGDFLAEGGGVR 16


RESULT 2
FIBA_CEREL
ID   FIBA_CEREL     STANDARD;      PRT;    19 AA.
AC   P14446;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Cervus elaphus (Red deer), and
OS   Cervus elaphus nelsoni (American elk).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860, 9864;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=C.elaphus;
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=C.e.nelsoni;
RA   Mross G.A., Doolittle R.F.;
RT   "Amino acid sequence studies on artiodacty fibrinopeptides.";
RL   Arch. Biochem. Biophys. 122:674-684(1967).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     19       FIBRINOPEPTIDE A.
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  1808 MW;  9BA54C26873B59C5 CRC64;

  Query Match             87.7%;  Score 57;  DB 1;  Length 19;
  Best Local Similarity   84.6%;  Pred. No. 0.00041;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
           : ||||||||||||
Db       7 ASSDFLAEGGGVR 19


RESULT 3
FIBA_HUMAN
ID   FIBA_HUMAN     STANDARD;      PRT;    866 AA.
AC   P02671; Q9BX62; Q9UCH2;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha/alpha-E chain precursor [Contains: Fibrinopeptide A].
GN   FGA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ALPHA-E FORM).
RX   MEDLINE=93090725; PubMed=1457396;
RA   Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
RA   Roy S.N., Redman C.M., Grieninger G.;
RT   "Carboxy-terminal-extended variant of the human fibrinogen alpha
RT   subunit: a novel exon conferring marked homology to beta and gamma
RT   subunits.";
RL   Biochemistry 31:11968-11972(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ALPHA-E FORM).
RA   Chung D.W., Grieninger G.;
RT   "Fibrinogen DNA and protein sequences.";
RL   (In) Ebert R.F. (eds.);
RL   Index of variant human fibrinogens, pp.13-24, CRC Press,
RL   Boca Raton (1994).
RN   [3]
RP   SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND
RP   ALA-456.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-655 FROM N.A. (ALPHA-E FORM).
RC   TISSUE=Liver;
RX   MEDLINE=91344740; PubMed=2102623;
RA   Chung D.W., Harris J.E., Davie E.W.;
RT   "Nucleotide sequences of the three genes coding for human
RT   fibrinogen.";
RL   Adv. Exp. Med. Biol. 281:39-48(1990).
RN   [5]
RP   SEQUENCE FROM N.A. (ALPHA FORM).
RX   MEDLINE=83247396; PubMed=6575389;
RA   Kant J.A., Lord S.T., Crabtree G.R.;
RT   "Partial mRNA sequences for human A alpha, B beta, and gamma
RT   fibrinogen chains: evolutionary and functional implications.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
RN   [6]
RP   SEQUENCE OF 1-629 FROM N.A.
RX   MEDLINE=83283432; PubMed=6688355;
RA   Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
RT   "Characterization of a complementary deoxyribonucleic acid coding for
RT   the alpha chain of human fibrinogen.";
RL   Biochemistry 22:3237-3244(1983).
RN   [7]
RP   SEQUENCE OF 20-629.
RA   Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT   "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RT   structural variants.";
RL   (In) Peeters H. (eds.);
RL   Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RL   Pergamon Press, Oxford (1980).
RN   [8]
RP   SEQUENCE OF 20-629, AND DISULFIDE BONDS.
RX   MEDLINE=80088231; PubMed=518846;
RA   Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
RT   "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT   Overlapping sequences providing the complete sequence.";
RL   Biochemistry 18:5410-5416(1979).
RN   [9]
RP   SEQUENCE OF 110-156 FROM N.A.
RX   MEDLINE=84069777; PubMed=6689067;
RA   Imam A.M., Eaton M.A., Williamson R., Humphries S.;
RT   "Isolation and characterisation of cDNA clones for the A alpha- and
RT   gamma-chains of human fibrinogen.";
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RL   Nucleic Acids Res. 11:7427-7434(1983).
RN   [10]
RP   SEQUENCE OF 605-644 FROM N.A. (ALPHA FORM).
RX   MEDLINE=83254384; PubMed=6575700;
RA   Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
RT   "Cloning of fibrinogen genes and their cDNA.";
RL   Ann. N.Y. Acad. Sci. 408:449-456(1983).
RN   [11]
RP   SEQUENCE OF 20-35.
RA   Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT   "Studies on fibrinopeptides from primates.";
RL   Acta Chem. Scand. 19:1788-1789(1965).
RN   [12]
RP   CROSS-LINKING ACCEPTOR SITES.
RX   MEDLINE=80088230; PubMed=518845;
RA   Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
RT   "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT   Exact location of cross-linking acceptor sites.";
RL   Biochemistry 18:5405-5410(1979).
RN   [13]
RP   CROSS-LINKING ACCEPTOR SITES.
RX   MEDLINE=78130085; PubMed=632262;
RA   Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;
RT   "Localization of the alpha-chain cross-link acceptor sites of human
RT   fibrin.";
RL   J. Biol. Chem. 253:2184-2195(1978).
RN   [14]
RP   VARIANT, AND DISULFIDE BONDS.
RX   MEDLINE=76225080; PubMed=936108;
RA   Blombaeck B., Hessel B., Hogg D.;
RT   "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RL   Thromb. Res. 8:639-658(1976).
RN   [15]
RP   REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX   MEDLINE=84305751; PubMed=6383194;
RA   Doolittle R.F.;
RT   "Fibrinogen and fibrin.";
RL   Annu. Rev. Biochem. 53:195-229(1984).
RN   [16]
RP   CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
RX   MEDLINE=87057190; PubMed=2877981;
RA   Kimura S., Aoki N.;
RT   "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";
RL   J. Biol. Chem. 261:15591-15595(1986).
RN   [17]
RP   PHOSPHORYLATION.
RX   MEDLINE=84104274; PubMed=6318767;
RA   Itarte E., Plana M., Guasch M.D., Martos C.;
RT   "Phosphorylation of fibrinogen by casein kinase 1.";
RL   Biochem. Biophys. Res. Commun. 117:631-636(1983).
RN   [18]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-39.
RX   MEDLINE=92218459; PubMed=1560020;
RA   Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RT   "The structure of residues 7-16 of the A alpha-chain of human
RT   fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL   J. Biol. Chem. 267:7911-7920(1992).
RN   [19]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 130-216.
RX   MEDLINE=97472408; PubMed=9333233;
RA   Spraggon G., Everse S.J., Doolittle R.F.;
RT   "Crystal structures of fragment D from human fibrinogen and its
RT   crosslinked counterpart from fibrin.";
RL   Nature 389:455-462(1997).
RN   [20]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
RX   MEDLINE=98292395; PubMed=9628725;
RA   Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT   "Crystal structure of fragment double-D from human fibrin with two
RT   different bound ligands.";
RL   Biochemistry 37:8637-8642(1998).
RN   [21]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.
RX   MEDLINE=98356117; PubMed=9689040;
RA   Spraggon G., Applegate D., Everse S.J., Zhang J.Z., Veerapandian L.,
RA   Redman C., Doolittle R.F., Grieninger G.;
RT   "Crystal structure of a recombinant alphaEC domain from human
RT   fibrinogen-420.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:9099-9104(1998).
RN   [22]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=99175089; PubMed=10074346;
RA   Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT   "Conformational changes in fragments D and double-D from human
RT   fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RL   Biochemistry 38:2941-2946(1999).
RN   [23]
RP   VARIANT KYOTO-2.
RX   MEDLINE=91300048; PubMed=2070049;
RA   Yoshida N., Okuma M., Hirata H., Matsuda M., Yamazumi K., Asakura S.;
RT   "Fibrinogen Kyoto II, a new congenitally abnormal molecule,
RT   characterized by the replacement of A alpha proline-18 by leucine.";
RL   Blood 78:149-153(1991).
RN   [24]
RP   VARIANT LIMA.
RX   MEDLINE=92340680; PubMed=1634621;
RA   Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA   Takahashi N., Arocha-Pinango C.L., Rodriguez S., Nagy H.,
RA   Perez-Requejo J.L., Matsuda M.;
RT   "Fibrinogen Lima: a homozygous dysfibrinogen with an A
RT   alpha-arginine-141 to serine substitution associated with extra
RT   N-glycosylation at A alpha-asparagine-139. Impaired fibrin gel
RT   formation but normal fibrin-facilitated plasminogen activation
RT   catalyzed by tissue-type plasminogen activator.";
RL   J. Clin. Invest. 90:67-76(1992).
RN   [25]
RP   VARIANT CARACAS-2.
RX   MEDLINE=91268018; PubMed=1675636;
RA   Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA   Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,
RA   Arocha-Pinango C.L., Matsuda M.;
RT   "An A alpha Ser-434 to N-glycosylated Asn substitution in a
RT   dysfibrinogen, fibrinogen Caracas II, characterized by impaired
RT   fibrin gel formation.";
RL   J. Biol. Chem. 266:11575-11581(1991).
RN   [26]
RP   VARIANT DUSART.
RX   MEDLINE=93232289; PubMed=8473507;
RA   Koopman J., Haverkate F., Grimbergen J., Lord S.T., Mosesson M.W.,
RA   Diorio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,
RA   Caen J.P.;
RT   "Molecular basis for fibrinogen Dusart (A alpha 554 Arg-->Cys) and
RT   its association with abnormal fibrin polymerization and
RT   thrombophilia.";

  Query Match             87.7%;  Score 57;  DB 1;  Length 866;
  Best Local Similarity   91.7%;  Pred. No. 0.021;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db      24 EGDFLAEGGGVR 35


RESULT 4
FIBA_CERSI
ID   FIBA_CERSI     STANDARD;      PRT;    16 AA.
AC   P14535;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
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OX   NCBI_TaxID=9807;
RN   [1]
RP   SEQUENCE.
RA   O'Neil P.B., Doolittle R.F.;
RT   "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL   Syst. Zool. 22:590-595(1973).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1639 MW;  0958CBB6293F4C81 CRC64;

  Query Match             86.2%;  Score 56;  DB 1;  Length 16;
  Best Local Similarity   76.9%;  Pred. No. 0.00052;
  Matches   10;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
           :| ||:|||||||
Db       4 TEGDFIAEGGGVR 16


RESULT 5
FIBA_TAPTE
ID   FIBA_TAPTE     STANDARD;      PRT;    16 AA.
AC   P14536;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Tapirus terrestris (Lowland tapir) (Brazilian tapir).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX   NCBI_TaxID=9801;
RN   [1]
RP   SEQUENCE.
RA   O'Neil P.B., Doolittle R.F.;
RT   "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL   Syst. Zool. 22:590-595(1973).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1622 MW;  48598EB6292F4030 CRC64;

  Query Match             83.1%;  Score 54;  DB 1;  Length 16;
  Best Local Similarity   76.9%;  Pred. No. 0.0012;
  Matches   10;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
           :| :|||||||||
Db       4 TEGEFLAEGGGVR 16


RESULT 6
FIBA_HYLLA
ID   FIBA_HYLLA     STANDARD;      PRT;    16 AA.
AC   P14453;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Hylobates lar (Common gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9580;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70294424; PubMed=5466708;
RA   Mross G.A., Doolittle R.F., Roberts B.F.;
RT   "Gibbon fibrinopeptides: identification of a glycine-serine allelism
RT   at position B-3.";
RL   Science 170:468-470(1970).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1565 MW;  49E98EB63EA04DD3 CRC64;

  Query Match             81.5%;  Score 53;  DB 1;  Length 16;
  Best Local Similarity   83.3%;  Pred. No. 0.0018;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | :||||||||||
Db       5 EGEFLAEGGGVR 16


RESULT 7
FIBA_CAMDR
ID   FIBA_CAMDR     STANDARD;      PRT;    18 AA.
AC   P14444;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Camelus dromedarius (Dromedary) (Arabian camel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX   NCBI_TaxID=9838;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=67209145; PubMed=6033721;
RA   Doolittle R.F., Schubert D., Schwartz S.A.;
RT   "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT   Dromedary camel, mule deer, and cape buffalo.";
RL   Arch. Biochem. Biophys. 118:456-467(1967).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     18       FIBRINOPEPTIDE A.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  1835 MW;  244448763D7F4CC6 CRC64;
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  Query Match             81.5%;  Score 53;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 0.002;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | :|||||||||
Db       7 EGEFLAEGGGVR 18


RESULT 8
FIBA_BISBO
ID   FIBA_BISBO     STANDARD;      PRT;    19 AA.
AC   P14441;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Bison bonasus (European bison).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bison.
OX   NCBI_TaxID=9902;
RN   [1]
RP   SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     19       FIBRINOPEPTIDE A.
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  1836 MW;  9BA55A0F473B59C5 CRC64;

  Query Match             81.5%;  Score 53;  DB 1;  Length 19;
  Best Local Similarity   76.9%;  Pred. No. 0.0021;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
           :  ||||||||||
Db       7 ASGDFLAEGGGVR 19


RESULT 9
FIBA_CERNI
ID   FIBA_CERNI     STANDARD;      PRT;    19 AA.
AC   P14447;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Cervus nippon (Sika deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9863;
RN   [1]
RP   SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J., Holmberg E.;
RT   "Structure of fibrinopeptides-its relation to enzyme specificity and
RT   phylogeny and classification of species.";
RL   Ark. Kemi 25:411-428(1966).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   NON_TER       19     19
SQ   SEQUENCE   19 AA;  1822 MW;  9BA40926873B59C5 CRC64;

  Query Match             81.5%;  Score 53;  DB 1;  Length 19;
  Best Local Similarity   76.9%;  Pred. No. 0.0021;
  Matches   10;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
           : |:||||||||||
Db       7 ASSEFLAEGGGVR 19


RESULT 10
FIBA_FELCA
ID   FIBA_FELCA     STANDARD;      PRT;    16 AA.
AC   P14450;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1620 MW;  C3C98EB62D6CC7D3 CRC64;

  Query Match             78.5%;  Score 51;  DB 1;  Length 16;
  Best Local Similarity   75.0%;  Pred. No. 0.004;
  Matches    9;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | :|:|||||||
Db       5 EGEFIAEGGGVR 16


RESULT 11
FIBA_CANFA
ID   FIBA_CANFA     STANDARD;      PRT;    28 AA.
AC   P02673; P14464;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Canis familiaris (Dog), and
OS   Vulpes vulpes (Red fox).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615, 9627;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=C.familiaris;
RX   MEDLINE=76081726; PubMed=1198547;
RA   Birken S., Wilner G.D., Canfield R.E.;
RT   "Studies of the structure of canine fibrinogen.";
RL   Thromb. Res. 7:599-610(1975).
RN   [2]
RP   SEQUENCE OF 1-16.
RC   SPECIES=C.familiaris, and V.vulpes;
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [3]
RP   SEQUENCE OF 1-16.
RC   SPECIES=C.familiaris;
RX   MEDLINE=66020594; PubMed=5836555;
RA   Osbahr A.J. Jr., Colman R.W., Laki K., Gladner J.A.;
RT   "The nature of the peptides released from canine fibrinogen.";
RL   Biochem. Biophys. Res. Commun. 14:555-558(1964).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR   PIR; A03118; A03118.
DR   PIR; A05296; A05296.
KW   Blood coagulation; Plasma; Phosphorylation.
FT   PEPTIDE        1     16       FIBRINOPEPTIDE A.
FT   MOD_RES        3      3       PHOSPHORYLATION (IN SOME MOLECULES).
FT   CONFLICT       2      2       N -> D (IN REF. 2).
FT   CONFLICT       4      7       KEGE -> EGKQ (IN REF. 2).
FT   NON_TER       28     28
SQ   SEQUENCE   28 AA;  2958 MW;  09DCD3F923BFEBD2 CRC64;

  Query Match             78.5%;  Score 51;  DB 1;  Length 28;
  Best Local Similarity   75.0%;  Pred. No. 0.0072;
  Matches    9;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           | :|:||||||||
Db       5 EGEFIAEGGGVR 16


RESULT 12
FIBA_PIG
ID   FIBA_PIG       STANDARD;      PRT;    17 AA.
AC   P14460;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   PEPTIDE        1     16       FIBRINOPEPTIDE A.
FT   NON_TER       17     17
SQ   SEQUENCE   17 AA;  1762 MW;  232EFEBB8B6B0A0C CRC64;

  Query Match             75.4%;  Score 49;  DB 1;  Length 17;
  Best Local Similarity   75.0%;  Pred. No. 0.0098;
  Matches    9;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           : :|||||||||
Db       6 KGEFLAEGGGVR 17


RESULT 13
FIBA_LAMGL
ID   FIBA_LAMGL     STANDARD;      PRT;    18 AA.
AC   P14454;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Lama glama (Llama), and
OS   Lama vicugna (Vicugna) (Vicugna vicugna).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX   NCBI_TaxID=9844, 9843;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=L.glama;
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=L.vicugna;
RA   Mross G.A., Doolittle R.F.;
RT   "Amino acid sequence studies on artiodacty fibrinopeptides.";
RL   Arch. Biochem. Biophys. 122:674-684(1967).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   PEPTIDE        1     18       FIBRINOPEPTIDE A.
FT   NON_TER       18     18
SQ   SEQUENCE   18 AA;  1834 MW;  2444487B8B7F4CC6 CRC64;

  Query Match             75.4%;  Score 49;  DB 1;  Length 18;
  Best Local Similarity   75.0%;  Pred. No. 0.01;
  Matches    9;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           : :|||||||||
Db       7 KGEFLAEGGGVR 18


RESULT 14
FIBA_SYNCA
ID   FIBA_SYNCA     STANDARD;      PRT;    15 AA.
AC   P14463;
DT   01-JAN-1990 (Rel. 13, Created)
```

```
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Syncerus caffer (Cape buffalo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Syncerus.
OX   NCBI_TaxID=9970;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=67209145; PubMed=6033721;
RA   Doolittle R.F., Schubert D., Schwartz S.A.;
RT   "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT   Dromedary camel, mule deer, and cape buffalo.";
RL   Arch. Biochem. Biophys. 118:456-467(1967).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     15       FIBRINOPEPTIDE A.
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1480 MW;  4E998EA5F0B41CC6 CRC64;

  Query Match             73.8%;  Score 48;  DB 1;  Length 15;
  Best Local Similarity   90.0%;  Pred. No. 0.013;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 DFLAEGGGVR 13
           :|||||||||
Db       6 EFLAEGGGVR 15


RESULT 15
FIBA_EQUAS
ID   FIBA_EQUAS     STANDARD;      PRT;    16 AA.
AC   P14449;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Equus asinus (Donkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9793;
RN   [1]
RP   SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1696 MW;  09598EB63C2A5957 CRC64;

  Query Match             73.8%;  Score 48;  DB 1;  Length 16;
  Best Local Similarity   66.7%;  Pred. No. 0.014;
  Matches    8;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
             | :|::||||||
Db       5 EGEFISEGGGVR 16


Search completed: February 10, 2003, 16:01:06
Job time : 12 secs
```

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 15:57:51 ; Search time 92 Seconds
(without alignments)
29.115 Million cell updates/sec

Title: US-09-845-729-1
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	87.7	218	4	Q8WW76	Q8ww76 homo sapien
2	46	70.8	557	11	Q99K47	Q99k47 mus musculu
3	43	66.2	260	10	Q8S2N9	Q8s2n9 oryza sativ
4	41	63.1	242	5	Q8T925	Q8t925 tetrahymena
5	41	63.1	552	2	Q9APX1	Q9apx1 pseudomonas
6	40	61.5	280	16	Q99WM6	Q99wm6 staphylococ
7	40	61.5	630	13	Q8UW15	Q8uw15 lapemis har
8	40	61.5	852	5	Q9U4G5	Q9u4g5 drosophila
9	39	60.0	89	16	Q98F73	Q98f73 rhizobium l
10	39	60.0	171	3	Q9P8L5	Q9p8l5 botrytis ci
11	39	60.0	186	2	Q9F7D5	Q9f7d5 salmonella
12	39	60.0	245	16	Q8Z6K4	Q8z6k4 salmonella
13	39	60.0	245	16	Q9Z4S4	Q9z4s4 salmonella
14	39	60.0	324	16	O53481	O53481 mycobacteri
15	39	60.0	465	10	Q9LH81	Q9lh81 arabidopsis
16	39	60.0	465	10	Q940V4	Q940v4 arabidopsis
17	39	60.0	481	10	Q8W0R4	Q8w0r4 sorghum bic
18	39	60.0	546	5	Q9VHD0	Q9vhd0 drosophila
19	39	60.0	705	2	O85866	O85866 sphingomona
20	39	60.0	748	10	Q8W0N1	Q8w0n1 oryza sativ
21	39	60.0	753	10	Q9LIC9	Q9lic9 arabidopsis
22	39	60.0	1159	4	Q9NY34	Q9ny34 homo sapien
23	39	60.0	1165	4	Q9NZQ8	Q9nzq8 homo sapien
24	38.5	59.2	741	16	Q8UFY1	Q8ufy1 agrobacteri
25	38	58.5	99	16	Q8ZQ92	Q8zq92 salmonella
26	38	58.5	147	10	Q9MAV0	Q9mav0 arabidopsis
27	38	58.5	256	16	Q92LM7	Q92lm7 rhizobium m
28	38	58.5	440	4	Q9UH99	Q9uh99 homo sapien
29	38	58.5	575	10	Q9LZM8	Q9lzm8 arabidopsis
30	38	58.5	611	4	Q8WYK5	Q8wyk5 homo sapien
31	38	58.5	652	16	Q8YPV7	Q8ypv7 anabaena sp
32	38	58.5	669	17	Q9YFF9	Q9yff9 aeropyrum p
33	38	58.5	686	10	Q9T0B3	Q9t0b3 arabidopsis
34	38	58.5	722	10	Q8VYR4	Q8vyr4 arabidopsis
35	38	58.5	727	10	Q9T0B4	Q9t0b4 arabidopsis
36	38	58.5	730	10	O22989	O22989 arabidopsis
37	38	58.5	742	4	O75156	O75156 homo sapien
38	38	58.5	770	10	O22988	O22988 arabidopsis
39	38	58.5	1458	12	Q8QTB8	Q8qtb8 white spot
40	38	58.5	2330	12	Q91L86	Q91186 white spot
41	38	58.5	4180	12	Q8VAQ8	Q8vaq8 white spot
42	37	56.9	79	10	Q8RUJ7	Q8ruj7 helianthus
43	37	56.9	127	3	Q9HGG0	Q9hgg0 cryptococcu
44	37	56.9	127	3	Q9HGF9	Q9hgf9 cryptococcu
45	37	56.9	135	3	Q9HGG3	Q9hgg3 cryptococcu

ALIGNMENTS

RESULT 1
Q8WW76
ID Q8WW76 PRELIMINARY; PRT; 218 AA.
AC Q8WW76;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to fibrinogen, A alpha polypeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC020764; AAH20764.1; -.
SQ SEQUENCE 218 AA; 24695 MW; 36D756A8116EA94A CRC64;

Query Match 87.7%; Score 57; DB 4; Length 218;
Best Local Similarity 91.7%; Pred. No. 0.033;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2 ESDFLAEGGGVR 13
           | ||||||||||
Db      24 EGDFLAEGGGVR 35
```

RESULT 2
Q99K47
ID Q99K47 PRELIMINARY; PRT; 557 AA.
AC Q99K47;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibrinogen A alpha polypeptide.
GN FGA.
OS Mus musculus (Mouse).

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005467; AAH05467.1; -.
DR   HSSP; P02671; 1FZA.
DR   MGD; MGI:1316726; Fga.
SQ   SEQUENCE   557 AA;  61325 MW;  C47F496D1BA432DE CRC64;

  Query Match             70.8%;  Score 46;  DB 11;  Length 557;
  Best Local Similarity   66.7%;  Pred. No. 8.4;
  Matches    8;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ESDFLAEGGGVR 13
           : :||:||||||
Db      25 KGEFLSEGGGVR 36


RESULT 3
Q8S2N9
ID   Q8S2N9      PRELIMINARY;      PRT;   260 AA.
AC   Q8S2N9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   B1066G12.16 protein.
GN   B1066G12.16.
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT   clone:B1066G12.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP003201; BAB89442.1; -.
SQ   SEQUENCE   260 AA;  29524 MW;  40929C6C486F0F06 CRC64;

  Query Match             66.2%;  Score 43;  DB 10;  Length 260;
  Best Local Similarity   69.2%;  Pred. No. 13;
  Matches    9;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
           |||| :||| |:|
Db     188 SESDPVAEGSGLR 200


RESULT 4
Q8T925
ID   Q8T925      PRELIMINARY;      PRT;   242 AA.
AC   Q8T925;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Igr2p.
GN   IGR2.
OS   Tetrahymena thermophila.
OC   Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC   Tetrahymenina; Tetrahymena.
OX   NCBI_TaxID=5911;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Turkewitz A.P., Haddad A.;
RT   "A non-architectural cargo protein in Tetrahymena thermophila dense
RT   core secretory granules.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY075152; AAL79515.1; -.
SQ   SEQUENCE   242 AA;  27000 MW;  A1E687237B618E8A CRC64;

  Query Match             63.1%;  Score 41;  DB 5;  Length 242;
  Best Local Similarity   70.0%;  Pred. No. 26;
  Matches    7;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGG 10
           |::||:||||
Db      77 SKNDFIAEGG 86


RESULT 5
Q9APX1
ID   Q9APX1      PRELIMINARY;      PRT;   552 AA.
AC   Q9APX1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Putative amino acid transport protein.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21142509; PubMed=11208781;
RA   Liang X., Pham X.Q.T., Olson M.V., Lory S.;
RT   "Identification of a Genomic Island Present in the Majority of
RT   Pathogenic Isolates of Pseudomonas aeruginosa.";
RL   J. Bacteriol. 183:843-853(2001).
DR   EMBL; AF241171; AAK01502.1; -.
DR   InterPro; IPR001734; Na/solut_symport.
DR   Pfam; PF00474; SSF; 1.
DR   TIGRFAMs; TIGR00813; sss; 1.
DR   PROSITE; PS00456; NA_SOLUT_SYMP_1; UNKNOWN_1.
DR   PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
SQ   SEQUENCE   552 AA;  58956 MW;  7A45F15BC8865C09 CRC64;

  Query Match             63.1%;  Score 41;  DB 2;  Length 552;
  Best Local Similarity   53.8%;  Pred. No. 65;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
           | :|| : |||:|
Db      58 STADFYSAGGGIR 70


RESULT 6
Q99WM6
ID   Q99WM6      PRELIMINARY;      PRT;   280 AA.
AC   Q99WM6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein SAV0351.
GN   SAV0351 OR SA0339.
OS   Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS   Staphylococcus aureus (strain N315).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC   Staphylococcus.
OX   NCBI_TaxID=158878, 158879;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX   MEDLINE=21311952; PubMed=11418146;
RA   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA   Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA   Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA   Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA   Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA   Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA   Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
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RT   "Whole genome sequencing of meticillin-resistant Staphylococcus
RT   aureus.";
RL   Lancet 357:1225-1240(2001).
DR   EMBL; AP003359; BAB56513.1; -.
DR   EMBL; AP003130; BAB41563.1; -.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transportr.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transportr; 1.
DR   SMART; SM00382; AAA; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   280 AA;  31464 MW;  2B0B9CF79F341652 CRC64;

  Query Match             61.5%;  Score 40;  DB 16;  Length 280;
  Best Local Similarity   66.7%;  Pred. No. 47;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 DFLAEGGGV 12
           ||:|:|||:
Db     176 DFVAQGGGI 184


RESULT 7
Q8UW15
ID   Q8UW15      PRELIMINARY;      PRT;   630 AA.
AC   Q8UW15;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Eukaryotic translation inititation factor 4B.
GN   EIF4B.
OS   Lapemis hardwickii (Hardwick's sea snake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Elapidae; Hydrophiinae; Lapemis.
OX   NCBI_TaxID=8781;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Xu A., Wei J., Yang W., Zhao G., Zhong X.;
RT   "A novel eukaryotic translation initiation factor 4B cDNA clone from
RT   sea snake.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF165225; AAL54908.1; -.
DR   InterPro; IPR000504; RNA_rec_mot.
DR   Pfam; PF00076; rrm; 1.
DR   SMART; SM00360; RRM; 1.
DR   PROSITE; PS50102; RRM; 1.
DR   PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SQ   SEQUENCE   630 AA;  71186 MW;  E3457B6ED3502A16 CRC64;

  Query Match             61.5%;  Score 40;  DB 13;  Length 630;
  Best Local Similarity   88.9%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 SDFLAEGGG 11
           |||||| ||
Db      18 SDFLAEDGG 26


RESULT 8
Q9U4G5
ID   Q9U4G5      PRELIMINARY;      PRT;   852 AA.
AC   Q9U4G5; Q9VQB2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   BCDNA:GH09817 protein.
GN   BCDNA:GH09817 OR CG4272.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RA   Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
RA   Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C.,
RA   Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
RA   Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
RA   Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
RA   Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
RA   Celniker S.E.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003583; AAF51264.1; ALT_INIT.
DR   EMBL; AF181640; AAD55426.1; -.
DR   FlyBase; FBgn0028485; BcDNA:GH09817.
KW   Hypothetical protein.
SQ   SEQUENCE   852 AA;  91073 MW;  B87C3607203DA4EC CRC64;

  Query Match             61.5%;  Score 40;  DB 5;  Length 852;
  Best Local Similarity   63.6%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGG 11
           || |:|:|| |
Db     376 SEEDYLSEGSG 386


RESULT 9
Q98F73
ID   Q98F73      PRELIMINARY;      PRT;    89 AA.
AC   Q98F73;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
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DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein msl3900.
GN   MSL3900.
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
DR   EMBL; AP003003; BAB50694.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   89 AA;  10058 MW;  5197B7CB06AFC351 CRC64;

  Query Match             60.0%;  Score 39;  DB 16;  Length 89;
  Best Local Similarity   61.5%;  Pred. No. 20;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
           || :|:|  ||||
Db      25 SEVEFVATDGGVR 37


RESULT 10
Q9P8L5
ID   Q9P8L5      PRELIMINARY;      PRT;   171 AA.
AC   Q9P8L5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   ABC transporter-like protein (Fragment).
GN   BCATRJ.
OS   Botrytis cinerea (Botryotinia fuckeliana).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC   Helotiales; Sclerotiniaceae; Botryotinia.
OX   NCBI_TaxID=40559;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B05.10;
RA   Schoonbeek H., Vermeulen T., Hayashi K., De Waard M.A.;
RT   "Differential expression of membrane-bound transporters in Botrytis
RT   cinerea.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF238228; AAF64438.1; -.
DR   InterPro; IPR004147; ABC1.
DR   Pfam; PF03109; ABC1; 1.
FT   NON_TER       1       1
FT   NON_TER     171     171
SQ   SEQUENCE   171 AA;  19561 MW;  15515C19C9FBB1F9 CRC64;

  Query Match             60.0%;  Score 39;  DB 3;  Length 171;
  Best Local Similarity   70.0%;  Pred. No. 41;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 SDFLAEGGGV 12
           |||:  ||||
Db     159 SDFMENGGGV 168


RESULT 11
Q9F7D5
ID   Q9F7D5      PRELIMINARY;      PRT;   186 AA.
AC   Q9F7D5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 20.7 kDa protein (Fragment).
GN   NTT.
OS   Salmonella enterica subsp. enterica serovar Typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=90371;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RX   MEDLINE=21172862; PubMed=11274105;
RA   Price-Carter M., Tingey J., Bobik T.A., Roth J.R.;
RT   "The Alternative Electron Acceptor Tetrathionate Supports B12-
RT   Dependent Anaerobic Growth of Salmonella enterica Serovar Typhimurium
RT   on Ethanolamine or 1,2-Propanediol.";
RL   J. Bacteriol. 183:2463-2475(2001).
DR   EMBL; AF282268; AAG31761.1; -.
KW   Hypothetical protein.
FT   NON_TER     186     186
SQ   SEQUENCE   186 AA;  20711 MW;  6B5FE0B04E07CFA0 CRC64;

  Query Match             60.0%;  Score 39;  DB 2;  Length 186;
  Best Local Similarity   60.0%;  Pred. No. 45;
  Matches    6;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SDFLAEGGGV 12
           :|::|||||:
Db     102 ADYVAEGGGL 111


RESULT 12
Q8Z6K4
ID   Q8Z6K4      PRELIMINARY;      PRT;   245 AA.
AC   Q8Z6K4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Orf 245 protein.
GN   STY1741.
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
DR   EMBL; AL627271; CAD01984.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   245 AA;  27429 MW;  11BF3BA03D62E3E3 CRC64;

  Query Match             60.0%;  Score 39;  DB 16;  Length 245;
  Best Local Similarity   60.0%;  Pred. No. 61;
  Matches    6;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SDFLAEGGGV 12
           :|::|||||:
Db     102 ADYVAEGGGL 111
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RESULT 13
Q9Z4S4
ID   Q9Z4S4      PRELIMINARY;      PRT;   245 AA.
AC   Q9Z4S4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   ORF 245 protein (Putative cytoplasmic protein).
GN   ORF245 OR STM1381.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RX   MEDLINE=99157556; PubMed=10027966;
RA   Hensel M., Egelseer C., Nikolaus T.;
RT   "Molecular and functional analysis indicates a mosaic structure of
RT   Salmonella Pathogenicity Island 2.";
RL   Mol. Microbiol. 31:489-498(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RA   Hensel M., Hinsley A.P., Nikolaus T., Sawers G., Berks B.C.;
RT   "he genetic basis of tetrathionate respiration in Salmonella
RT   typhimurium.";
RL   Mol. Microbiol. 0:0-0(0).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
DR   EMBL; AJ224978; CAB37418.1; -.
DR   EMBL; AE008760; AAL20305.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   245 AA;  27430 MW;  FFBF31AA9DC8E943 CRC64;

  Query Match             60.0%;  Score 39;  DB 16;  Length 245;
  Best Local Similarity   60.0%;  Pred. No. 61;
  Matches    6;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SDFLAEGGGV 12
           :|::|||||:
Db     102 ADYVAEGGGL 111


RESULT 14
O53481
ID   O53481      PRELIMINARY;      PRT;   324 AA.
AC   O53481;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Putative transmembrane protein.
GN   RV2037C OR MT2097 OR MTV018.24C.
OS   Mycobacterium tuberculosis.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1773;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H37RV;
RX   MEDLINE=98295987; PubMed=9634230;
RA   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA   Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA   Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA   Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA   Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA   Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA   Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA   Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT   "Deciphering the biology of Mycobacterium tuberculosis from the
RT   complete genome sequence.";
RL   Nature 393:537-544(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CDC 1551 / OSHKOSH;
RA   Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA   Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA   Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA   Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA   Bishai W.;
RT   "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT   laboratory strains.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL021899; CAA17251.1; -.
DR   EMBL; AE007060; AAK46376.1; -.
DR   TIGR; MT2097; -.
DR   TubercuList; Rv2037c; -.
DR   InterPro; IPR002641; Patatin.
DR   Pfam; PF01734; Patatin; 1.
KW   Transmembrane; Complete proteome.
FT   CONFLICT    312    312       C -> Y (IN REF. 2).
SQ   SEQUENCE   324 AA;  34688 MW;  B8C8A4901E6D15FC CRC64;

  Query Match             60.0%;  Score 39;  DB 16;  Length 324;
  Best Local Similarity   70.0%;  Pred. No. 83;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 DFLAEGGGVR 13
             | : ||||||
Db      10 DLVCEGGGVR 19


RESULT 15
Q9LH81
ID   Q9LH81      PRELIMINARY;      PRT;   465 AA.
AC   Q9LH81;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Cytochrome P450.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RA   Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=20363099; PubMed=10907853;
RA   Nakamura Y.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT   Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT   TAC and BAC clones.";
RL   DNA Res. 7:217-221(2000).
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR   EMBL; AP002060; BAB02270.1; -.
DR   InterPro; IPR001128; Cytochrome_P450.
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DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW   Heme; Monooxygenase; Oxidoreductase.
SQ   SEQUENCE   465 AA;  53862 MW;  630A21D0765E0D0D CRC64;

  Query Match             60.0%;  Score 39;  DB 10;  Length 465;
  Best Local Similarity   69.2%;  Pred. No. 1.2e+02;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 SESDFLAEGGGVR 13
           |:| ||  |||||
Db     401 SKSYFLLFGGGVR 413


Search completed: February 10, 2003, 16:02:46
Job time : 95 secs
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